Full wwPDB EM Validation Report

Jul 7, 2021 – 11:23 am BST

PDB ID	:	7OI0
EMDB ID	:	EMD-12916
Title	:	E.coli delta rbfA pre-30S ribosomal subunit class D
Authors	:	Maksimova, E.; Korepanov, A.; Baymukhametov, T.; Kravchenko, O.; Stolboushkina, E.
Deposited on	:	2021-05-11
Resolution	:	2.76 Å(reported)
Based on initial model	:	4V4Q

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

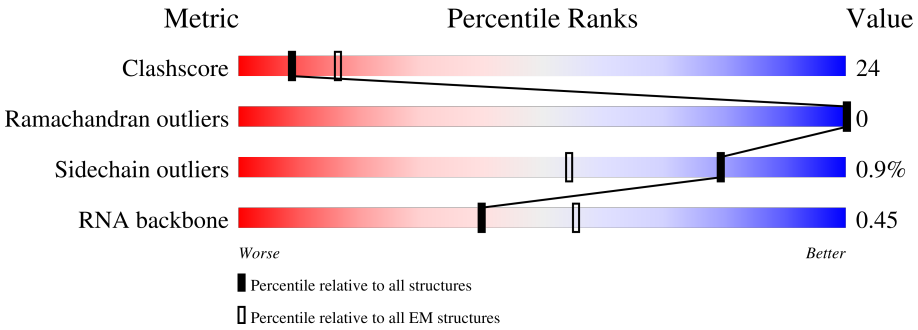
EMDB validation analysis	:	0.0.0.dev84
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.22

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.76 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	D	205	59% 40%
2	F	135	10% 33% 41% 26%
3	H	129	61% 39%
4	K	128	49% 39% 34% 26%
5	L	123	59% 41%
6	O	89	48% 51%
7	P	82	63% 35%

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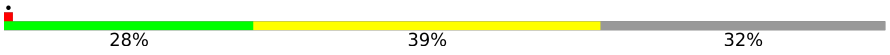
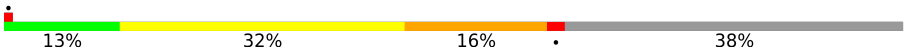
Mol	Chain	Length	Quality of chain
8	Q	83	
9	R	74	
10	T	86	
11	A	1542	

2 Entry composition

There are 12 unique types of molecules in this entry. The entry contains 29255 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	D	205	1643	1026	315	298	4	0	0

- Molecule 2 is a protein called 30S ribosomal protein S6, fully modified isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	F	100	817	515	148	148	6	0	0

- Molecule 3 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	H	129	979	616	173	184	6	0	0

- Molecule 4 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	K	95	702	433	137	130	2	0	0

- Molecule 5 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	L	123	955	590	196	165	4	0	0

- Molecule 6 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	O	88	716	440	146	129	1	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	79	ARG	GLN	conflict	UNP A0A4S5B232

- Molecule 7 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	P	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 8 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	Q	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 9 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	R	50	Total	C	N	O	0	0
			407	259	76	72		

- Molecule 10 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	T	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 11 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	A	963	Total	C	N	O	P	0	0
			20700	9228	3823	6686	963		

- Molecule 12 is water.

Mol	Chain	Residues	Atoms		AltConf
12	D	6	Total	O	0
			6	6	
12	L	4	Total	O	0
			4	4	
12	P	18	Total	O	0
			18	18	

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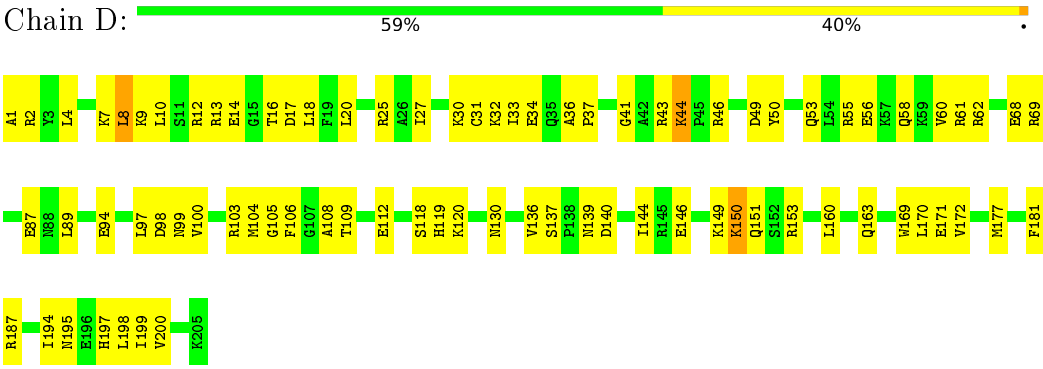
Mol	Chain	Residues	Atoms	AltConf
12	Q	3	Total O 3 3	0
12	T	6	Total O 6 6	0
12	A	337	Total O 337 337	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

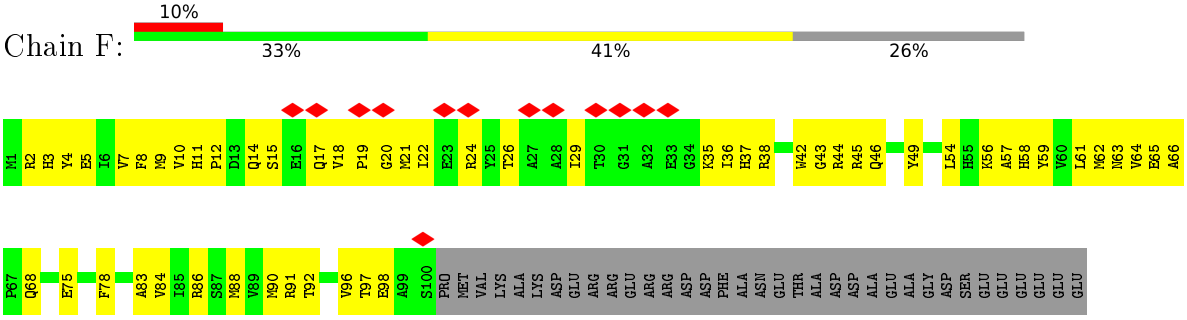
- Molecule 1: 30S ribosomal protein S4

Chain D:



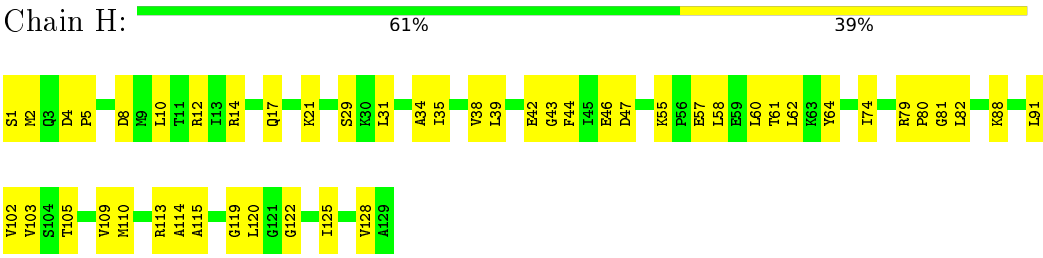
- Molecule 2: 30S ribosomal protein S6, fully modified isoform

Chain F:



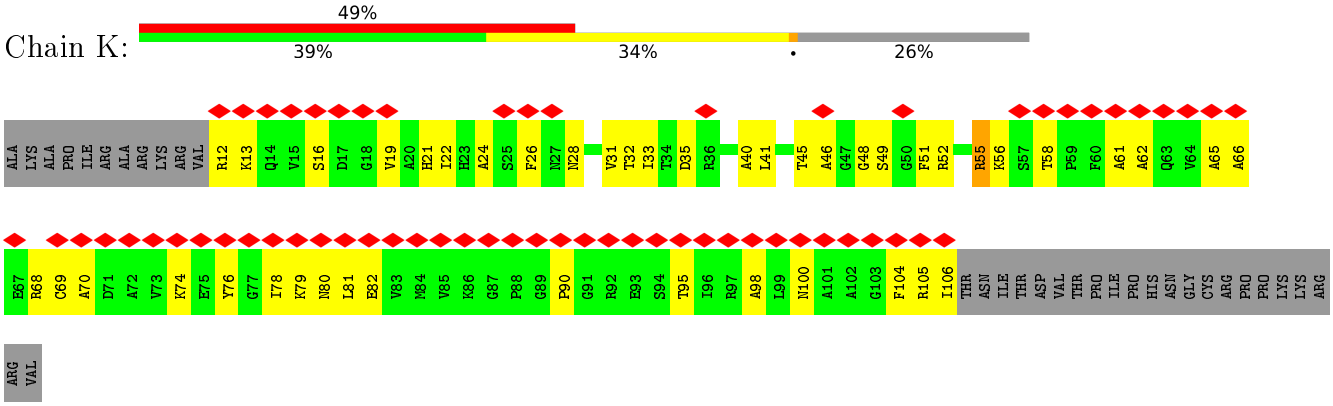
- Molecule 3: 30S ribosomal protein S8

Chain H:



- Molecule 4: 30S ribosomal protein S11

Chain K:

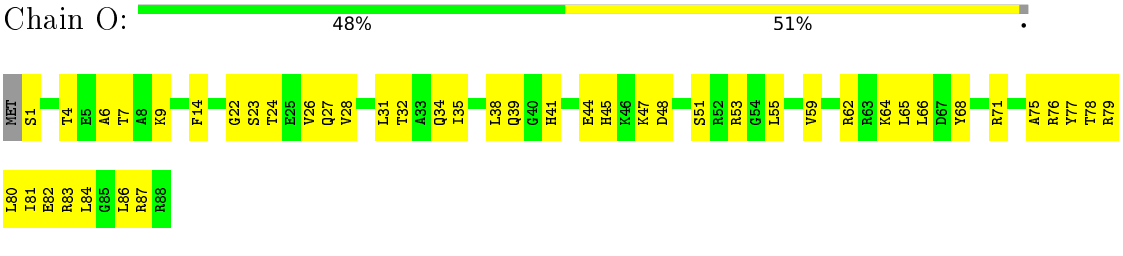


- Molecule 5: 30S ribosomal protein S12

Chain L:

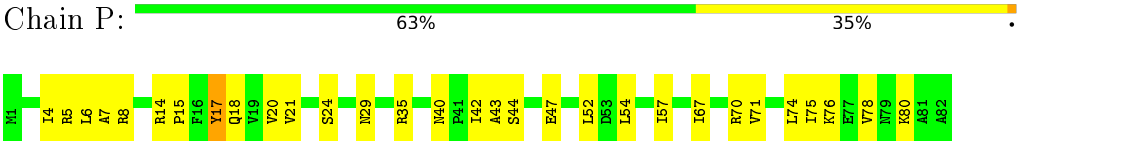
- Molecule 6: 30S ribosomal protein S15

Chain O:



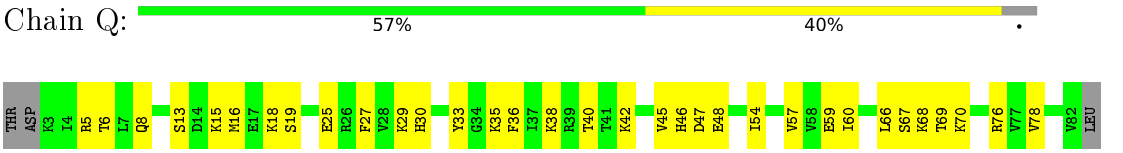
- Molecule 7: 30S ribosomal protein S16

Chain P:



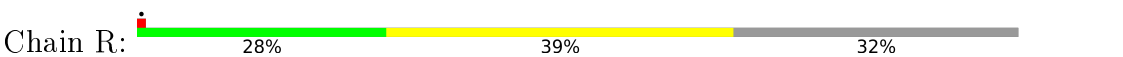
- Molecule 8: 30S ribosomal protein S17

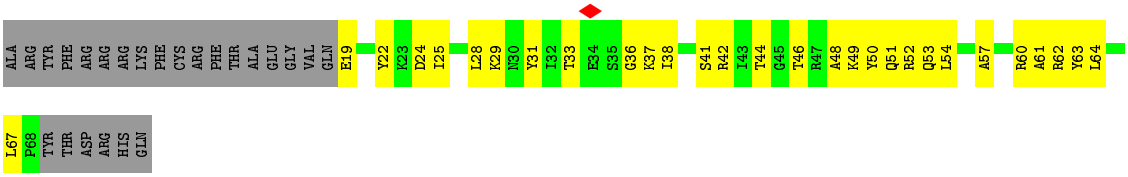
Chain Q:



- Molecule 9: 30S ribosomal protein S18

Chain R:



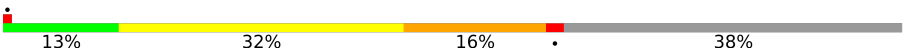


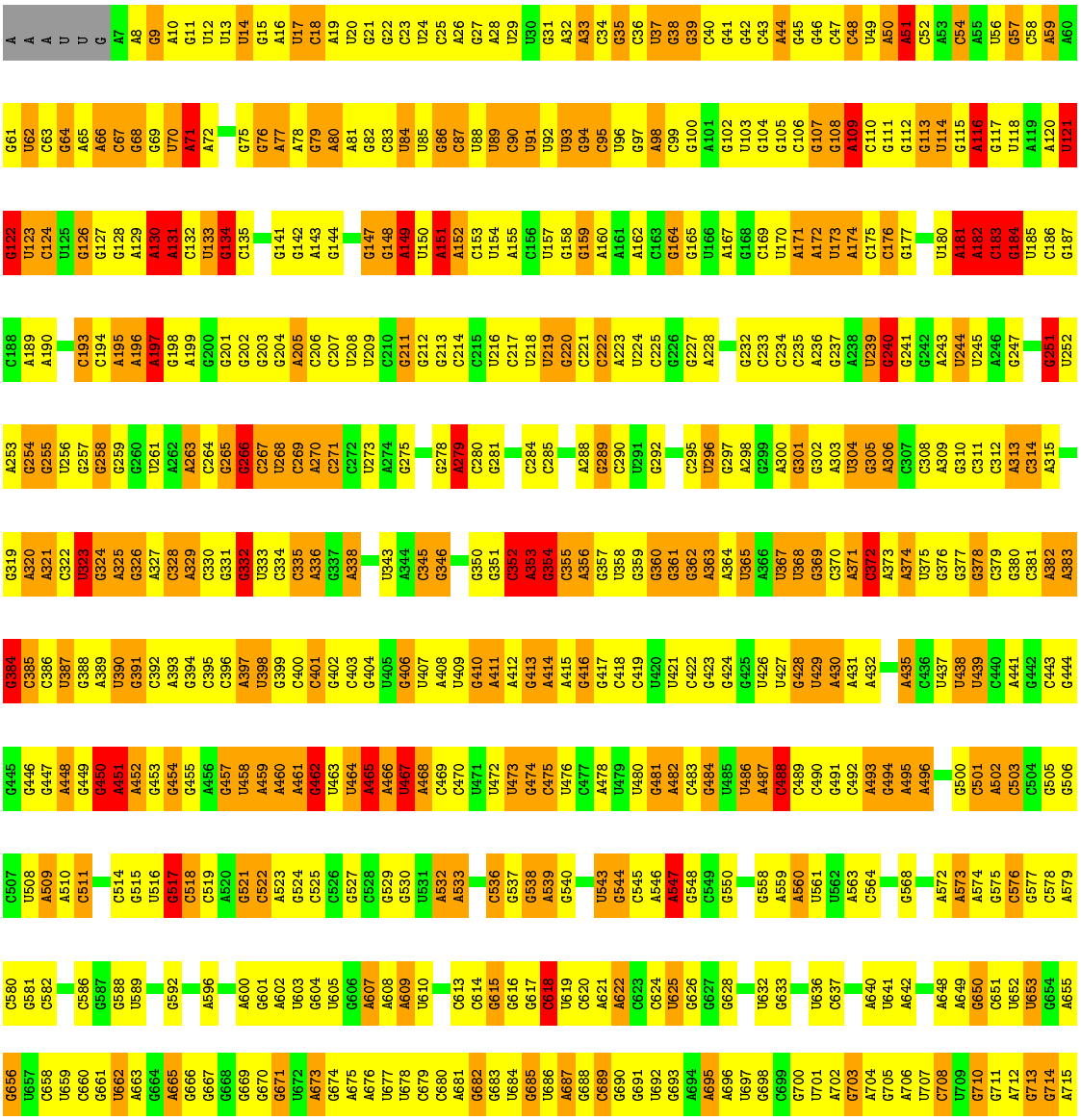
• Molecule 10: 30S ribosomal protein S20

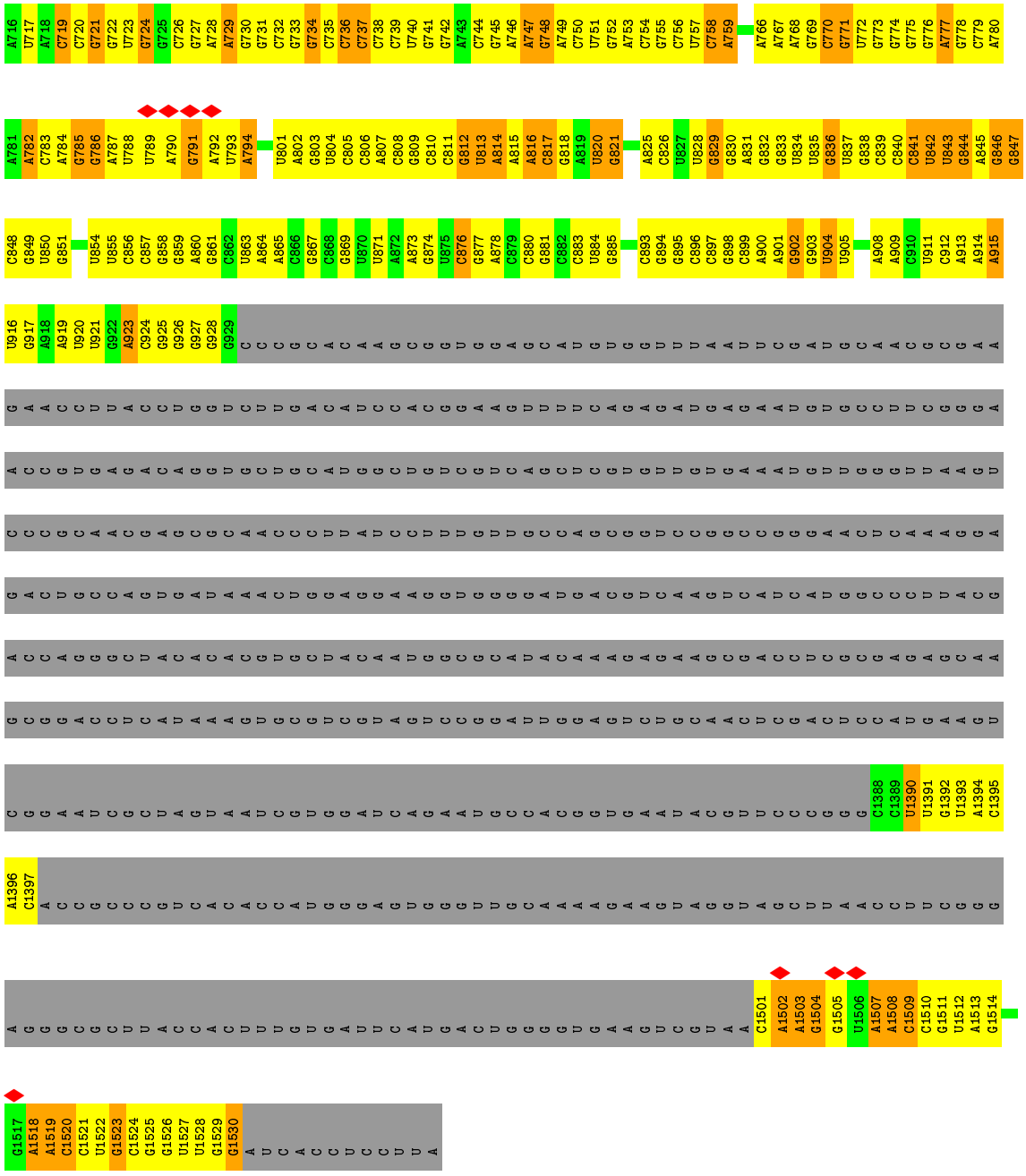
Chain T:

• Molecule 11: 16S rRNA

Chain A:







4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	106319	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	2.5	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	5.611	Depositor
Minimum map value	-2.640	Depositor
Average map value	0.007	Depositor
Map value standard deviation	0.083	Depositor
Recommended contour level	0.218	Depositor
Map size (Å)	378.4, 378.4, 378.4	wwPDB
Map dimensions	440, 440, 440	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.86, 0.86, 0.86	Depositor

5 Model quality

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	D	0.62	0/1665	0.67	0/2227
2	F	0.29	0/835	0.48	0/1128
3	H	0.47	0/989	0.61	0/1326
4	K	0.26	0/713	0.46	0/960
5	L	0.68	0/969	0.77	0/1300
6	O	0.41	0/724	0.53	0/966
7	P	1.03	2/659 (0.3%)	0.79	0/884
8	Q	0.80	0/657	0.68	0/881
9	R	0.25	0/412	0.46	0/553
10	T	0.66	0/671	0.69	0/888
11	A	1.71	381/23184 (1.6%)	1.20	132/36171 (0.4%)
All	All	1.50	383/31478 (1.2%)	1.10	132/47284 (0.3%)

All (383) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	A	452	A	N9-C4	-10.64	1.31	1.37
11	A	353	A	N9-C4	-10.25	1.31	1.37
11	A	355	C	N3-C4	-8.73	1.27	1.33
11	A	113	G	C6-N1	-8.63	1.33	1.39
11	A	394	G	C5-C4	-7.84	1.32	1.38
11	A	102	G	C6-N1	-7.76	1.34	1.39
11	A	322	C	N3-C4	-7.61	1.28	1.33
11	A	329	A	N7-C5	-7.57	1.34	1.39
11	A	152	A	N9-C4	-7.56	1.33	1.37
11	A	377	G	C2-N3	-7.49	1.26	1.32
11	A	354	G	C6-N1	-7.49	1.34	1.39
11	A	387	U	C2-N3	-7.49	1.32	1.37
11	A	391	G	C6-N1	-7.45	1.34	1.39
11	A	378	G	C8-N7	-7.33	1.26	1.30
11	A	324	G	C5-C4	-7.24	1.33	1.38
11	A	393	A	C5-C4	-7.18	1.33	1.38
11	A	449	G	C5-C4	-7.15	1.33	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	A	401	C	N3-C4	-7.12	1.28	1.33
11	A	450	G	C6-N1	-7.11	1.34	1.39
11	A	106	C	N1-C6	-7.10	1.32	1.37
11	A	61	G	C6-N1	-7.09	1.34	1.39
11	A	450	G	C5-C4	-7.04	1.33	1.38
11	A	107	G	N9-C8	-7.03	1.32	1.37
11	A	391	G	C8-N7	-7.01	1.26	1.30
11	A	310	G	C6-N1	-6.99	1.34	1.39
11	A	113	G	C5-C4	-6.97	1.33	1.38
11	A	618	C	N3-C4	-6.97	1.29	1.33
11	A	45	G	C5-C4	-6.96	1.33	1.38
11	A	354	G	C8-N7	-6.95	1.26	1.30
11	A	109	A	C8-N7	-6.94	1.26	1.31
11	A	378	G	C6-N1	-6.94	1.34	1.39
11	A	108	G	C5-C6	-6.92	1.35	1.42
11	A	117	G	C6-N1	-6.91	1.34	1.39
11	A	311	C	N3-C4	-6.87	1.29	1.33
11	A	379	C	N3-C4	-6.87	1.29	1.33
11	A	257	G	C6-N1	-6.84	1.34	1.39
11	A	390	U	C2-N3	-6.82	1.32	1.37
11	A	42	G	C5-C4	-6.81	1.33	1.38
11	A	384	G	N1-C2	-6.79	1.32	1.37
11	A	332	G	C8-N7	-6.76	1.26	1.30
11	A	181	A	C5-C4	-6.74	1.34	1.38
11	A	107	G	C8-N7	-6.71	1.26	1.30
11	A	357	G	C6-N1	-6.71	1.34	1.39
11	A	59	A	N9-C4	-6.71	1.33	1.37
11	A	393	A	N7-C5	-6.70	1.35	1.39
11	A	35	G	C8-N7	-6.70	1.26	1.30
11	A	112	G	C5-C4	-6.70	1.33	1.38
11	A	402	G	C6-N1	-6.67	1.34	1.39
11	A	113	G	C8-N7	-6.66	1.26	1.30
11	A	391	G	N7-C5	-6.63	1.35	1.39
11	A	449	G	C2-N3	-6.60	1.27	1.32
11	A	127	G	C6-N1	-6.57	1.34	1.39
11	A	46	G	C6-N1	-6.57	1.34	1.39
11	A	292	G	C8-N7	-6.57	1.27	1.30
11	A	54	C	N1-C6	-6.56	1.33	1.37
11	A	66	A	C6-N1	-6.55	1.30	1.35
11	A	369	G	C6-N1	-6.54	1.34	1.39
11	A	112	G	C8-N7	-6.50	1.27	1.30
11	A	117	G	C5-C4	-6.50	1.33	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	A	403	C	C2-N3	-6.50	1.30	1.35
11	A	133	U	C2-N3	-6.49	1.33	1.37
11	A	392	C	N3-C4	-6.49	1.29	1.33
11	A	182	A	N9-C4	-6.47	1.33	1.37
11	A	354	G	C2-N3	-6.44	1.27	1.32
11	A	393	A	N9-C8	-6.37	1.32	1.37
11	A	43	C	N3-C4	-6.35	1.29	1.33
11	A	109	A	N7-C5	-6.35	1.35	1.39
11	A	546	A	N9-C4	-6.35	1.34	1.37
11	A	353	A	N3-C4	-6.34	1.31	1.34
11	A	37	U	C2-N3	-6.32	1.33	1.37
11	A	625	U	C2-N3	-6.30	1.33	1.37
11	A	255	G	C6-N1	-6.28	1.35	1.39
11	A	370	C	N3-C4	-6.24	1.29	1.33
11	A	488	C	N1-C6	-6.24	1.33	1.37
11	A	38	G	C5-C4	-6.23	1.33	1.38
11	A	384	G	C8-N7	-6.22	1.27	1.30
11	A	624	C	N3-C4	-6.22	1.29	1.33
11	A	292	G	C5-C4	-6.21	1.33	1.38
11	A	45	G	C6-N1	-6.21	1.35	1.39
11	A	108	G	N9-C4	-6.19	1.32	1.38
11	A	609	A	N9-C4	-6.14	1.34	1.37
11	A	322	C	N1-C6	-6.13	1.33	1.37
11	A	326	G	C5-C4	-6.12	1.34	1.38
11	A	371	A	C2-N3	-6.12	1.28	1.33
11	A	107	G	C5-C4	-6.12	1.34	1.38
11	A	61	G	C2-N3	-6.11	1.27	1.32
11	A	354	G	C5-C6	-6.11	1.36	1.42
11	A	112	G	C6-N1	-6.11	1.35	1.39
11	A	371	A	C5-C4	-6.11	1.34	1.38
11	A	108	G	N7-C5	-6.10	1.35	1.39
11	A	548	G	C6-N1	-6.10	1.35	1.39
11	A	323	U	C2-N3	-6.10	1.33	1.37
11	A	378	G	C2-N3	-6.09	1.27	1.32
11	A	362	G	C5-C4	-6.09	1.34	1.38
11	A	240	G	C6-N1	-6.09	1.35	1.39
11	A	263	A	N9-C4	-6.07	1.34	1.37
11	A	377	G	C5-C4	-6.07	1.34	1.38
11	A	389	A	C6-N6	-6.06	1.29	1.33
11	A	57	G	C6-N1	-6.05	1.35	1.39
11	A	54	C	C2-N3	-6.05	1.30	1.35
11	A	312	C	C4-C5	-6.05	1.38	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	A	181	A	N9-C4	-6.04	1.34	1.37
11	A	393	A	N9-C4	-6.04	1.34	1.37
11	A	449	G	C6-N1	-6.03	1.35	1.39
11	A	378	G	C5-C4	-6.03	1.34	1.38
11	A	232	G	C2-N3	-6.01	1.27	1.32
11	A	113	G	N1-C2	-6.01	1.32	1.37
11	A	42	G	C6-N1	-6.01	1.35	1.39
11	A	331	G	C8-N7	-6.00	1.27	1.30
11	A	222	C	N1-C6	-6.00	1.33	1.37
11	A	392	C	C2-N3	-6.00	1.30	1.35
11	A	233	C	N3-C4	-6.00	1.29	1.33
11	A	388	G	C6-N1	-5.99	1.35	1.39
11	A	326	G	C8-N7	-5.99	1.27	1.30
11	A	356	A	C5-C4	-5.99	1.34	1.38
11	A	290	C	N3-C4	-5.98	1.29	1.33
11	A	292	G	C6-N1	-5.98	1.35	1.39
11	A	42	G	C2-N3	-5.98	1.27	1.32
11	A	402	G	C5-C4	-5.98	1.34	1.38
11	A	404	G	C5-C4	-5.97	1.34	1.38
11	A	41	G	C2-N3	-5.97	1.27	1.32
11	A	263	A	C5-C4	-5.96	1.34	1.38
11	A	41	G	C6-N1	-5.95	1.35	1.39
11	A	482	A	N7-C5	-5.95	1.35	1.39
11	A	377	G	C6-N1	-5.94	1.35	1.39
11	A	391	G	C2-N3	-5.94	1.27	1.32
11	A	324	G	N1-C2	-5.93	1.33	1.37
11	A	289	G	C8-N7	-5.93	1.27	1.30
11	A	135	C	N3-C4	-5.92	1.29	1.33
11	A	360	G	C2-N3	-5.92	1.28	1.32
11	A	271	C	C2-N3	-5.91	1.31	1.35
11	A	308	C	N3-C4	-5.91	1.29	1.33
11	A	354	G	N7-C5	-5.90	1.35	1.39
11	A	325	A	C5-C4	-5.90	1.34	1.38
11	A	305	G	C8-N7	-5.89	1.27	1.30
11	A	181	A	C8-N7	-5.88	1.27	1.31
11	A	124	C	N3-C4	-5.86	1.29	1.33
11	A	330	C	N3-C4	-5.86	1.29	1.33
11	A	384	G	C6-N1	-5.84	1.35	1.39
11	A	69	G	C8-N7	-5.84	1.27	1.30
11	A	193	C	N1-C6	-5.84	1.33	1.37
11	A	621	A	N7-C5	-5.84	1.35	1.39
11	A	59	A	C8-N7	-5.83	1.27	1.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	A	360	G	C5-C4	-5.83	1.34	1.38
11	A	402	G	N1-C2	-5.83	1.33	1.37
11	A	495	A	N7-C5	-5.83	1.35	1.39
11	A	109	A	N9-C8	-5.81	1.33	1.37
11	A	358	U	N3-C4	-5.81	1.33	1.38
11	A	117	G	N1-C2	-5.81	1.33	1.37
11	A	147	G	C6-N1	-5.80	1.35	1.39
11	A	369	G	C8-N7	-5.80	1.27	1.30
11	A	128	G	C8-N7	-5.79	1.27	1.30
11	A	481	G	C6-N1	-5.79	1.35	1.39
11	A	371	A	C6-N1	-5.78	1.31	1.35
11	A	372	C	N3-C4	-5.77	1.29	1.33
11	A	223	A	N9-C4	-5.77	1.34	1.37
11	A	46	G	C5-C4	-5.76	1.34	1.38
11	A	501	C	N3-C4	-5.76	1.29	1.33
11	A	392	C	N1-C6	-5.74	1.33	1.37
11	A	451	A	N9-C4	-5.74	1.34	1.37
11	A	503	C	N3-C4	-5.74	1.29	1.33
11	A	251	G	C5-C4	5.74	1.42	1.38
11	A	377	G	C8-N7	-5.74	1.27	1.30
11	A	134	G	C8-N7	-5.73	1.27	1.30
11	A	241	G	C5-C4	-5.72	1.34	1.38
11	A	175	C	N3-C4	-5.71	1.29	1.33
11	A	332	G	C5-C4	-5.71	1.34	1.38
11	A	617	G	C5-C4	-5.71	1.34	1.38
11	A	240	G	C2-N3	-5.70	1.28	1.32
11	A	395	C	N3-C4	-5.70	1.29	1.33
7	P	20	VAL	CB-CG2	-5.69	1.40	1.52
11	A	268	U	C2-N3	-5.69	1.33	1.37
11	A	354	G	C5-C4	-5.69	1.34	1.38
11	A	361	G	C2-N3	-5.69	1.28	1.32
11	A	501	C	N1-C6	-5.68	1.33	1.37
11	A	41	G	C5-C4	-5.68	1.34	1.38
11	A	543	U	C2-N3	-5.68	1.33	1.37
11	A	289	G	C6-N1	-5.68	1.35	1.39
11	A	269	C	C4-C5	-5.67	1.38	1.43
11	A	234	C	C2-N3	-5.65	1.31	1.35
11	A	196	A	N3-C4	-5.64	1.31	1.34
11	A	380	G	C5-C4	-5.64	1.34	1.38
11	A	271	C	N1-C2	-5.63	1.34	1.40
11	A	52	C	N3-C4	-5.62	1.30	1.33
11	A	199	A	C8-N7	-5.62	1.27	1.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	A	451	A	N3-C4	-5.62	1.31	1.34
11	A	61	G	N1-C2	-5.61	1.33	1.37
11	A	448	A	N9-C4	-5.61	1.34	1.37
11	A	323	U	N3-C4	-5.61	1.33	1.38
11	A	45	G	C5-C6	-5.60	1.36	1.42
11	A	116	A	C6-N1	-5.60	1.31	1.35
11	A	326	G	C6-N1	-5.60	1.35	1.39
11	A	482	A	N9-C4	-5.60	1.34	1.37
11	A	877	G	C5-C4	-5.59	1.34	1.38
11	A	175	C	C2-N3	-5.59	1.31	1.35
11	A	327	A	C5-C4	-5.59	1.34	1.38
11	A	395	C	C2-N3	-5.58	1.31	1.35
11	A	384	G	C5-C4	-5.58	1.34	1.38
11	A	451	A	N7-C5	-5.56	1.35	1.39
11	A	195	A	N9-C4	-5.55	1.34	1.37
11	A	326	G	N1-C2	-5.55	1.33	1.37
11	A	357	G	C2-N3	-5.55	1.28	1.32
11	A	143	A	N9-C4	-5.55	1.34	1.37
11	A	258	G	C6-N1	-5.55	1.35	1.39
11	A	329	A	C8-N7	-5.55	1.27	1.31
11	A	547	A	C5-C4	-5.54	1.34	1.38
11	A	257	G	C2-N3	-5.54	1.28	1.32
11	A	58	C	N1-C6	-5.54	1.33	1.37
11	A	222	C	N3-C4	-5.53	1.30	1.33
11	A	232	G	C5-C4	-5.52	1.34	1.38
11	A	107	G	N7-C5	-5.51	1.35	1.39
11	A	376	G	C6-N1	-5.51	1.35	1.39
11	A	386	C	N3-C4	-5.51	1.30	1.33
11	A	186	C	N3-C4	-5.50	1.30	1.33
11	A	374	A	C8-N7	-5.50	1.27	1.31
11	A	757	U	C2-N3	-5.50	1.33	1.37
11	A	314	C	C4-C5	-5.49	1.38	1.43
11	A	610	U	C2-N3	-5.48	1.33	1.37
11	A	69	G	C6-N1	-5.48	1.35	1.39
11	A	315	A	C8-N7	-5.48	1.27	1.31
11	A	222	C	C4-C5	-5.47	1.38	1.43
11	A	42	G	N1-C2	-5.47	1.33	1.37
11	A	550	G	C5-C4	-5.47	1.34	1.38
11	A	117	G	C8-N7	-5.46	1.27	1.30
11	A	332	G	N7-C5	-5.46	1.35	1.39
11	A	41	G	N1-C2	-5.46	1.33	1.37
11	A	108	G	N3-C4	-5.46	1.31	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	A	102	G	C2-N3	-5.45	1.28	1.32
11	A	758	C	N1-C6	-5.45	1.33	1.37
11	A	107	G	C2-N3	-5.44	1.28	1.32
11	A	122	G	C5-C4	-5.44	1.34	1.38
11	A	489	C	N1-C6	-5.44	1.33	1.37
11	A	131	A	N3-C4	-5.43	1.31	1.34
11	A	171	A	N7-C5	-5.43	1.35	1.39
11	A	197	A	C5-C4	-5.43	1.34	1.38
11	A	361	G	C5-C4	-5.42	1.34	1.38
11	A	273	U	C2-N3	-5.42	1.33	1.37
11	A	228	A	N7-C5	-5.42	1.35	1.39
7	P	17	TYR	CD1-CE1	-5.42	1.31	1.39
11	A	64	G	C5-C4	-5.42	1.34	1.38
11	A	45	G	N1-C2	-5.41	1.33	1.37
11	A	62	U	C2-N3	-5.41	1.33	1.37
11	A	386	C	N1-C6	-5.41	1.33	1.37
11	A	184	G	C2-N3	-5.41	1.28	1.32
11	A	539	A	N9-C4	-5.40	1.34	1.37
11	A	481	G	N7-C5	-5.39	1.36	1.39
11	A	331	G	C5-C4	-5.39	1.34	1.38
11	A	502	A	C6-N1	-5.38	1.31	1.35
11	A	319	G	C6-N1	-5.38	1.35	1.39
11	A	40	C	N3-C4	-5.37	1.30	1.33
11	A	270	A	C6-N1	-5.37	1.31	1.35
11	A	143	A	C8-N7	-5.37	1.27	1.31
11	A	261	U	C2-N3	-5.36	1.33	1.37
11	A	402	G	C5-C6	-5.36	1.36	1.42
11	A	373	A	C6-N1	-5.36	1.31	1.35
11	A	501	C	C2-N3	-5.35	1.31	1.35
11	A	371	A	C8-N7	-5.35	1.27	1.31
11	A	39	G	C6-N1	-5.34	1.35	1.39
11	A	111	G	C8-N7	-5.34	1.27	1.30
11	A	391	G	C5-C6	-5.34	1.37	1.42
11	A	104	G	C5-C4	-5.33	1.34	1.38
11	A	353	A	C5-C6	-5.33	1.36	1.41
11	A	259	G	C6-N1	-5.33	1.35	1.39
11	A	378	G	N1-C2	-5.32	1.33	1.37
11	A	622	A	N9-C4	-5.32	1.34	1.37
11	A	289	G	C5-C4	-5.30	1.34	1.38
11	A	352	C	C2-N3	-5.30	1.31	1.35
11	A	545	C	N3-C4	-5.30	1.30	1.33
11	A	310	G	C5-C4	-5.30	1.34	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	A	362	G	N9-C4	-5.30	1.33	1.38
11	A	35	G	C6-N1	-5.29	1.35	1.39
11	A	44	A	N7-C5	-5.29	1.36	1.39
11	A	120	A	N9-C4	-5.29	1.34	1.37
11	A	279	A	N9-C4	-5.29	1.34	1.37
11	A	304	U	C2-N3	-5.28	1.34	1.37
11	A	142	G	C6-N1	-5.28	1.35	1.39
11	A	338	A	N9-C4	-5.28	1.34	1.37
11	A	147	G	C8-N7	-5.27	1.27	1.30
11	A	54	C	C4-C5	-5.27	1.38	1.43
11	A	123	U	C2-N3	-5.26	1.34	1.37
11	A	175	C	N1-C6	-5.26	1.33	1.37
11	A	313	A	C2-N3	-5.26	1.28	1.33
11	A	357	G	C5-C4	-5.25	1.34	1.38
11	A	378	G	N3-C4	-5.25	1.31	1.35
11	A	393	A	C8-N7	-5.25	1.27	1.31
11	A	149	A	N9-C4	-5.24	1.34	1.37
11	A	391	G	C5-C4	-5.24	1.34	1.38
11	A	331	G	C2-N3	-5.23	1.28	1.32
11	A	357	G	C8-N7	-5.23	1.27	1.30
11	A	41	G	C8-N7	-5.23	1.27	1.30
11	A	175	C	C4-C5	-5.23	1.38	1.43
11	A	389	A	N9-C8	-5.22	1.33	1.37
11	A	104	G	C6-N1	-5.22	1.35	1.39
11	A	224	U	C2-N3	-5.22	1.34	1.37
11	A	550	G	C2-N3	-5.21	1.28	1.32
11	A	131	A	C6-N1	-5.21	1.31	1.35
11	A	45	G	C8-N7	-5.20	1.27	1.30
11	A	220	G	C5-C4	-5.19	1.34	1.38
11	A	387	U	N3-C4	-5.19	1.33	1.38
11	A	196	A	C5-C4	-5.18	1.35	1.38
11	A	265	G	C5-C4	-5.18	1.34	1.38
11	A	223	A	C5-C4	-5.18	1.35	1.38
11	A	313	A	C5-C4	-5.18	1.35	1.38
11	A	617	G	C8-N7	-5.18	1.27	1.30
11	A	142	G	C5-C4	-5.17	1.34	1.38
11	A	174	A	N9-C4	-5.17	1.34	1.37
11	A	354	G	N3-C4	-5.16	1.31	1.35
11	A	59	A	C5-C4	-5.16	1.35	1.38
11	A	199	A	C6-N1	-5.16	1.31	1.35
11	A	368	U	C2-N3	-5.15	1.34	1.37
11	A	502	A	C5-C6	-5.15	1.36	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	A	487	A	N7-C5	-5.15	1.36	1.39
11	A	326	G	N7-C5	-5.15	1.36	1.39
11	A	114	U	C2-N3	-5.14	1.34	1.37
11	A	40	C	C2-N3	-5.14	1.31	1.35
11	A	174	A	N3-C4	-5.14	1.31	1.34
11	A	323	U	C5-C6	-5.14	1.29	1.34
11	A	333	U	C2-N3	-5.14	1.34	1.37
11	A	391	G	N9-C8	-5.13	1.34	1.37
11	A	172	A	C6-N1	-5.13	1.31	1.35
11	A	385	C	N1-C6	-5.13	1.34	1.37
11	A	510	A	N9-C4	-5.12	1.34	1.37
11	A	141	G	N7-C5	-5.12	1.36	1.39
11	A	448	A	N3-C4	-5.12	1.31	1.34
11	A	450	G	C2-N3	-5.12	1.28	1.32
11	A	197	A	N3-C4	-5.12	1.31	1.34
11	A	628	G	N1-C2	-5.12	1.33	1.37
11	A	388	G	C8-N7	-5.11	1.27	1.30
11	A	482	A	C8-N7	-5.11	1.27	1.31
11	A	176	C	N3-C4	-5.11	1.30	1.33
11	A	484	G	C8-N7	-5.11	1.27	1.30
11	A	36	C	N3-C4	-5.11	1.30	1.33
11	A	482	A	C6-N1	-5.10	1.31	1.35
11	A	64	G	N1-C2	-5.10	1.33	1.37
11	A	382	A	C5-C4	-5.10	1.35	1.38
11	A	610	U	C2-O2	-5.10	1.17	1.22
11	A	181	A	C5-C6	-5.10	1.36	1.41
11	A	481	G	N9-C8	-5.10	1.34	1.37
11	A	127	G	C5-C4	-5.09	1.34	1.38
11	A	484	G	C2-N3	-5.09	1.28	1.32
11	A	320	A	C2-N3	-5.09	1.28	1.33
11	A	126	G	C6-N1	-5.09	1.35	1.39
11	A	105	G	N9-C4	-5.08	1.33	1.38
11	A	240	G	C5-C4	-5.08	1.34	1.38
11	A	324	G	C6-N1	-5.08	1.35	1.39
11	A	547	A	N9-C4	-5.08	1.34	1.37
11	A	402	G	C2-N3	-5.08	1.28	1.32
11	A	227	G	C2-N3	-5.07	1.28	1.32
11	A	324	G	N9-C8	-5.07	1.34	1.37
11	A	375	U	C2-N3	-5.07	1.34	1.37
11	A	393	A	C6-N1	-5.07	1.31	1.35
11	A	377	G	N3-C4	-5.07	1.31	1.35
11	A	544	G	C6-N1	-5.07	1.36	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	A	326	G	C2-N3	-5.06	1.28	1.32
11	A	254	G	C6-N1	-5.05	1.36	1.39
11	A	450	G	N9-C8	-5.05	1.34	1.37
11	A	270	A	C5-C6	-5.05	1.36	1.41
11	A	324	G	C2-N3	-5.04	1.28	1.32
11	A	360	G	N7-C5	-5.04	1.36	1.39
11	A	383	A	N7-C5	-5.04	1.36	1.39
11	A	327	A	N9-C8	-5.04	1.33	1.37
11	A	544	G	C5-C4	-5.03	1.34	1.38
11	A	621	A	C5-C6	-5.03	1.36	1.41
11	A	68	G	C2-N3	-5.03	1.28	1.32
11	A	111	G	N9-C8	-5.03	1.34	1.37
11	A	193	C	N3-C4	-5.03	1.30	1.33
11	A	538	G	C6-N1	-5.03	1.36	1.39
11	A	151	A	N9-C4	-5.02	1.34	1.37
11	A	51	A	N7-C5	-5.02	1.36	1.39
11	A	313	A	C8-N7	-5.02	1.28	1.31
11	A	380	G	N9-C8	-5.02	1.34	1.37
11	A	130	A	C5-C4	-5.02	1.35	1.38
11	A	447	G	N9-C8	-5.02	1.34	1.37
11	A	358	U	C2-N3	-5.01	1.34	1.37
11	A	376	G	N7-C5	-5.01	1.36	1.39
11	A	265	G	C8-N7	-5.01	1.27	1.30
11	A	367	U	C2-N3	-5.01	1.34	1.37
11	A	374	A	C6-N1	-5.01	1.32	1.35
11	A	454	G	C5-C4	-5.01	1.34	1.38
11	A	51	A	N9-C8	-5.01	1.33	1.37
11	A	391	G	C6-O6	-5.01	1.19	1.24
11	A	401	C	C4-C5	-5.00	1.39	1.43
11	A	452	A	N7-C5	-5.00	1.36	1.39

All (132) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	A	108	G	C4-C5-N7	15.57	117.03	110.80
11	A	108	G	C5-N7-C8	-12.91	97.84	104.30
11	A	108	G	C6-C5-N7	-12.81	122.71	130.40
11	A	452	A	C2-N3-C4	-10.97	105.11	110.60
11	A	452	A	N3-C4-C5	10.44	134.11	126.80
11	A	452	A	N3-C4-N9	-10.38	119.09	127.40
11	A	108	G	N1-C6-O6	10.31	126.08	119.90
11	A	182	A	O4'-C1'-N9	9.96	116.16	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	A	372	C	C6-N1-C2	-9.63	116.45	120.30
11	A	108	G	C5-C6-O6	-9.15	123.11	128.60
11	A	181	A	O4'-C1'-N9	9.10	115.48	108.20
11	A	182	A	C5-N7-C8	-8.86	99.47	103.90
11	A	353	A	C5-N7-C8	-8.54	99.63	103.90
11	A	108	G	N7-C8-N9	8.36	117.28	113.10
11	A	511	C	N1-C2-O2	-8.33	113.90	118.90
11	A	462	G	C4-N9-C1'	8.29	137.28	126.50
11	A	462	G	C8-N9-C1'	-8.04	116.55	127.00
11	A	108	G	C4-N9-C1'	8.00	136.90	126.50
11	A	610	U	N3-C2-O2	-7.93	116.65	122.20
11	A	736	C	N3-C2-O2	-7.80	116.44	121.90
11	A	266	G	N9-C4-C5	-7.71	102.32	105.40
11	A	108	G	N9-C4-C5	-7.70	102.32	105.40
11	A	108	G	C8-N9-C1'	-7.62	117.09	127.00
11	A	182	A	N7-C8-N9	7.55	117.58	113.80
11	A	396	C	N3-C4-C5	7.49	124.90	121.90
11	A	708	C	N3-C2-O2	-7.38	116.73	121.90
11	A	383	A	C8-N9-C4	-7.22	102.91	105.80
11	A	383	A	N7-C8-N9	7.20	117.40	113.80
11	A	736	C	N1-C2-O2	7.10	123.16	118.90
11	A	353	A	C4-C5-N7	7.06	114.23	110.70
11	A	462	G	C6-C5-N7	-7.06	126.16	130.40
11	A	181	A	C8-N9-C4	7.05	108.62	105.80
11	A	266	G	C8-N9-C4	6.96	109.18	106.40
11	A	314	C	N3-C4-C5	6.87	124.65	121.90
11	A	452	A	C6-N1-C2	6.84	122.71	118.60
11	A	517	G	C5-C6-O6	-6.81	124.52	128.60
11	A	279	A	C2-N3-C4	-6.80	107.20	110.60
11	A	496	A	O4'-C1'-N9	6.68	113.54	108.20
11	A	353	A	O4'-C1'-N9	6.62	113.50	108.20
11	A	332	G	C5-C6-O6	-6.58	124.65	128.60
11	A	328	C	P-O3'-C3'	6.54	127.55	119.70
11	A	462	G	C4-C5-N7	6.46	113.38	110.80
11	A	737	C	N3-C2-O2	-6.41	117.41	121.90
11	A	416	G	C4'-C3'-O3'	6.30	125.61	113.00
11	A	269	C	N3-C4-C5	6.28	124.41	121.90
11	A	152	A	C5-N7-C8	-6.27	100.77	103.90
11	A	354	G	C4-C5-N7	6.24	113.30	110.80
11	A	416	G	C3'-C2'-C1'	6.19	106.45	101.50
11	A	915	A	N1-C6-N6	-6.19	114.89	118.60
11	A	266	G	C5-C6-N1	-6.17	108.41	111.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	A	462	G	N7-C8-N9	6.13	116.17	113.10
11	A	181	A	N9-C4-C5	-6.09	103.36	105.80
11	A	353	A	C2-N3-C4	-6.06	107.57	110.60
11	A	332	G	N1-C6-O6	6.04	123.52	119.90
11	A	786	G	N1-C6-O6	-6.03	116.28	119.90
11	A	465	A	C8-N9-C4	-6.03	103.39	105.80
11	A	465	A	C3'-C2'-C1'	-6.02	96.68	101.50
11	A	708	C	N1-C2-O2	5.99	122.50	118.90
11	A	538	G	C4-C5-N7	5.98	113.19	110.80
11	A	124	C	C6-N1-C2	-5.97	117.91	120.30
11	A	452	A	C4-C5-C6	-5.96	114.02	117.00
11	A	543	U	N3-C2-O2	-5.96	118.03	122.20
11	A	311	C	C6-N1-C2	-5.93	117.93	120.30
11	A	462	G	C5-N7-C8	-5.85	101.38	104.30
11	A	462	G	N9-C4-C5	-5.83	103.07	105.40
11	A	403	C	N3-C4-C5	5.82	124.23	121.90
11	A	610	U	C6-N1-C2	-5.81	117.52	121.00
11	A	876	C	N3-C4-C5	5.80	124.22	121.90
11	A	372	C	N3-C4-C5	-5.78	119.59	121.90
11	A	416	G	N9-C1'-C2'	-5.78	105.65	112.00
11	A	37	U	C2-N3-C4	-5.77	123.54	127.00
11	A	193	C	C5-C6-N1	-5.75	118.13	121.00
11	A	52	C	C6-N1-C2	-5.70	118.02	120.30
11	A	474	G	O4'-C1'-N9	5.70	112.76	108.20
11	A	517	G	C4-C5-N7	5.68	113.07	110.80
11	A	266	G	N1-C6-O6	5.68	123.31	119.90
11	A	494	G	C4-C5-N7	5.68	113.07	110.80
11	A	266	G	C8-N9-C1'	-5.64	119.67	127.00
11	A	147	G	N9-C4-C5	-5.63	103.15	105.40
11	A	219	U	N3-C4-O4	-5.61	115.47	119.40
11	A	182	A	C4-C5-N7	5.60	113.50	110.70
11	A	121	U	N1-C2-O2	5.59	126.71	122.80
11	A	355	C	N3-C4-N4	-5.58	114.09	118.00
11	A	219	U	C2-N1-C1'	-5.55	111.04	117.70
11	A	322	C	C5-C6-N1	-5.54	118.23	121.00
11	A	219	U	C5-C4-O4	5.51	129.20	125.90
11	A	438	U	O4'-C1'-N1	5.48	112.59	108.20
11	A	460	A	N9-C4-C5	-5.46	103.61	105.80
11	A	386	C	N3-C4-C5	5.45	124.08	121.90
11	A	452	A	C5-C6-N6	5.45	128.06	123.70
11	A	617	G	C8-N9-C4	5.44	108.58	106.40
11	A	148	G	C5-N7-C8	-5.42	101.59	104.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	A	465	A	N9-C1'-C2'	-5.41	106.05	112.00
11	A	269	C	C4-C5-C6	-5.41	114.70	117.40
11	A	108	G	N9-C1'-C2'	-5.40	106.06	112.00
11	A	365	U	O4'-C1'-N1	5.40	112.52	108.20
11	A	403	C	C2-N3-C4	-5.39	117.20	119.90
11	A	786	G	C5-C6-O6	5.38	131.83	128.60
11	A	221	C	N1-C2-O2	5.36	122.12	118.90
11	A	109	A	N1-C2-N3	-5.35	126.62	129.30
11	A	69	G	C8-N9-C1'	-5.33	120.08	127.00
11	A	103	U	N3-C2-O2	-5.29	118.50	122.20
11	A	175	C	N3-C4-C5	5.29	124.02	121.90
11	A	737	C	C6-N1-C2	-5.29	118.19	120.30
11	A	517	G	N1-C6-O6	5.28	123.07	119.90
11	A	54	C	N3-C4-C5	5.28	124.01	121.90
11	A	251	G	C5-C6-O6	5.27	131.76	128.60
11	A	69	G	N9-C4-C5	-5.26	103.30	105.40
11	A	365	U	C2-N1-C1'	5.25	124.00	117.70
11	A	467	U	C2-N1-C1'	5.24	123.98	117.70
11	A	332	G	C4-C5-N7	5.23	112.89	110.80
11	A	494	G	C5-C6-O6	-5.22	125.47	128.60
11	A	320	A	C8-N9-C4	5.22	107.89	105.80
11	A	465	A	C4'-C3'-O3'	5.21	123.41	113.00
11	A	121	U	N3-C2-O2	-5.20	118.56	122.20
11	A	332	G	N9-C4-C5	-5.20	103.32	105.40
11	A	467	U	N3-C2-O2	-5.18	118.57	122.20
11	A	356	A	O4'-C1'-N9	5.17	112.33	108.20
11	A	266	G	C6-C5-N7	-5.15	127.31	130.40
11	A	67	C	C2-N3-C4	-5.12	117.34	119.90
11	A	40	C	N3-C4-C5	5.12	123.95	121.90
11	A	353	A	N7-C8-N9	5.11	116.36	113.80
11	A	394	G	C5-C6-N1	5.11	114.05	111.50
11	A	183	C	P-O3'-C3'	5.10	125.82	119.70
11	A	586	C	N3-C4-C5	5.09	123.94	121.90
11	A	372	C	C5-C4-N4	5.08	123.76	120.20
11	A	109	A	N9-C4-C5	-5.08	103.77	105.80
11	A	71	A	C3'-C2'-C1'	5.05	105.54	101.50
11	A	379	C	N3-C4-C5	5.05	123.92	121.90
11	A	322	C	C6-N1-C2	5.04	122.32	120.30
11	A	354	G	C2-N3-C4	-5.02	109.39	111.90
11	A	54	C	O4'-C1'-N1	5.02	112.21	108.20

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	1643	0	1710	120	0
2	F	817	0	808	62	0
3	H	979	0	1034	50	0
4	K	702	0	702	41	0
5	L	955	0	1019	61	0
6	O	716	0	742	50	0
7	P	649	0	666	25	0
8	Q	648	0	691	33	0
9	R	407	0	438	26	0
10	T	665	0	714	23	0
11	A	20700	0	10405	711	0
12	A	337	0	0	22	0
12	D	6	0	0	0	0
12	L	4	0	0	0	0
12	P	18	0	0	3	0
12	Q	3	0	0	1	0
12	T	6	0	0	1	0
All	All	29255	0	18929	1094	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 24.

All (1094) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:31:CYS:SG	11:A:429:U:H5"	1.50	1.52
11:A:26:A:N6	11:A:558:G:N3	1.91	1.17
1:D:8:LEU:CD2	11:A:429:U:H3'	1.73	1.16
1:D:31:CYS:SG	11:A:429:U:C5'	2.36	1.12
11:A:411:A:C2	11:A:430:A:N6	2.17	1.11
1:D:9:LYS:HG3	1:D:37:PRO:CB	1.80	1.11
2:F:2:ARG:HG2	2:F:92:THR:CG2	1.82	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:8:LEU:HD22	11:A:429:U:C3'	1.84	1.07
1:D:8:LEU:HD23	1:D:31:CYS:SG	1.95	1.07
1:D:33:ILE:HG22	1:D:34:GLU:H	1.17	1.07
11:A:411:A:N1	11:A:430:A:N6	2.04	1.06
6:O:47:LYS:HE2	11:A:808:C:OP1	1.57	1.04
6:O:38:LEU:HD22	6:O:55:LEU:HD13	1.36	1.02
8:Q:13:SER:OG	8:Q:15:LYS:HD3	1.59	1.01
1:D:112:GLU:OE2	1:D:153:ARG:HD2	1.60	1.01
11:A:687:A:H62	11:A:703:G:N2	1.57	1.01
2:F:20:GLY:O	2:F:24:ARG:HG3	1.62	0.99
5:L:66:ILE:HD12	5:L:96:THR:HG21	1.46	0.98
11:A:76:G:H1	11:A:93:U:H3	1.09	0.97
11:A:448:A:N7	11:A:486:U:N3	2.13	0.97
11:A:663:A:H61	11:A:742:G:H1	1.13	0.96
11:A:836:G:H1	11:A:850:U:H3	0.99	0.96
11:A:444:G:N2	11:A:490:C:O2	1.98	0.96
11:A:411:A:N6	11:A:430:A:N7	2.13	0.96
1:D:108:ALA:H	1:D:112:GLU:HG2	1.32	0.95
11:A:457:G:N2	11:A:475:C:O2	1.98	0.95
11:A:335:C:HO2'	11:A:336:A:H8	0.96	0.95
11:A:148:G:H1	11:A:174:A:N6	1.62	0.94
2:F:2:ARG:HG2	2:F:92:THR:HG21	1.50	0.94
11:A:148:G:H1	11:A:174:A:H61	0.97	0.94
11:A:687:A:N6	11:A:703:G:H21	1.66	0.93
11:A:444:G:N1	11:A:490:C:N3	2.15	0.93
1:D:1:ALA:HB3	11:A:547:A:OP2	1.69	0.93
11:A:658:C:O2	11:A:748:G:N2	2.02	0.93
11:A:94:G:N2	11:A:97:G:N7	2.17	0.92
1:D:98:ASP:OD1	1:D:99:ASN:N	2.02	0.92
11:A:687:A:H62	11:A:703:G:H21	0.94	0.92
11:A:187:G:N2	11:A:190:A:N7	2.20	0.90
11:A:462:G:N1	11:A:470:C:N3	2.20	0.90
6:O:38:LEU:HD23	6:O:55:LEU:HB2	1.53	0.90
11:A:207:C:H5	12:A:1732:HOH:O	1.54	0.89
3:H:42:GLU:OE2	3:H:44:PHE:HD2	1.55	0.88
11:A:839:C:O2	11:A:847:G:N2	2.07	0.86
11:A:411:A:H2	11:A:430:A:N6	1.71	0.86
10:T:9:ARG:NH2	11:A:107:G:N7	2.23	0.85
1:D:9:LYS:HG3	1:D:37:PRO:HB2	1.55	0.85
1:D:1:ALA:CB	11:A:547:A:OP2	2.25	0.85
11:A:658:C:N3	11:A:748:G:N1	2.25	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:674:G:H2'	11:A:675:A:H8	1.42	0.84
2:F:18:VAL:O	2:F:22:ILE:HG13	1.77	0.84
11:A:839:C:N3	11:A:847:G:N1	2.24	0.84
11:A:682:G:H2'	11:A:683:G:C8	2.13	0.84
11:A:515:G:OP2	11:A:532:A:N6	2.11	0.83
11:A:152:A:N6	11:A:169:C:O2	2.11	0.83
1:D:8:LEU:HD22	11:A:429:U:H3'	0.89	0.83
11:A:202:G:HO2'	11:A:468:A:H8	1.25	0.83
11:A:113:G:N3	11:A:353:A:O2'	2.12	0.83
11:A:695:A:H61	11:A:786:G:H21	1.27	0.83
2:F:2:ARG:CG	2:F:92:THR:CG2	2.57	0.82
11:A:559:A:H4'	11:A:560:A:H3'	1.61	0.82
8:Q:68:LYS:HG2	8:Q:69:THR:HG23	1.62	0.82
11:A:148:G:N2	11:A:174:A:N1	2.28	0.82
11:A:465:A:N6	11:A:468:A:N7	2.26	0.82
11:A:116:A:C2	12:A:1649:HOH:O	2.32	0.82
2:F:2:ARG:HG2	2:F:92:THR:HG22	1.61	0.81
11:A:582:C:O2	11:A:759:A:N6	2.14	0.80
4:K:19:VAL:HG12	4:K:82:GLU:HB3	1.63	0.80
6:O:38:LEU:HD22	6:O:55:LEU:CD1	2.11	0.80
5:L:66:ILE:CD1	5:L:96:THR:HG21	2.09	0.80
6:O:38:LEU:CD2	6:O:55:LEU:HB2	2.12	0.80
1:D:8:LEU:HD23	11:A:429:U:H5'	1.62	0.80
11:A:79:G:N2	11:A:90:C:O2	2.13	0.80
11:A:86:G:H1'	11:A:87:C:H5	1.47	0.79
7:P:8:ARG:HD2	12:P:104:HOH:O	1.81	0.79
7:P:70:ARG:O	7:P:74:LEU:HG	1.82	0.79
11:A:17:U:H2'	11:A:18:C:C6	2.17	0.79
11:A:410:G:O6	11:A:429:U:O2'	1.98	0.79
11:A:697:U:H1'	11:A:785:G:H21	1.47	0.79
11:A:665:A:N7	11:A:724:G:O6	2.15	0.78
1:D:56:GLU:HG2	1:D:198:LEU:CD1	2.12	0.78
11:A:343:U:O2	11:A:346:G:N1	2.12	0.78
11:A:452:A:H62	11:A:480:U:H3	1.29	0.78
3:H:46:GLU:HB2	3:H:61:THR:HG23	1.64	0.78
1:D:8:LEU:CD2	1:D:31:CYS:SG	2.70	0.78
6:O:38:LEU:CD2	6:O:55:LEU:HD13	2.12	0.78
11:A:79:G:N1	11:A:90:C:N3	2.26	0.78
1:D:146:GLU:HA	1:D:149:LYS:HG3	1.64	0.78
11:A:766:A:H61	11:A:1511:G:H1'	1.48	0.78
11:A:26:A:H61	11:A:558:G:H1'	1.48	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:673:A:H2'	11:A:674:G:C8	2.19	0.77
11:A:769:G:H4'	11:A:1513:A:H4'	1.65	0.77
11:A:782:A:OP1	11:A:1514:G:N2	2.18	0.77
8:Q:27:PHE:CZ	8:Q:36:PHE:HB3	2.20	0.76
6:O:24:THR:HG23	6:O:65:LEU:HD12	1.66	0.76
11:A:116:A:H2	12:A:1649:HOH:O	1.65	0.76
11:A:462:G:O6	11:A:470:C:N4	2.16	0.76
2:F:17:GLN:HG3	2:F:21:MET:HG2	1.67	0.76
2:F:2:ARG:CG	2:F:92:THR:HG21	2.16	0.76
3:H:47:ASP:O	3:H:61:THR:HG22	1.86	0.76
11:A:766:A:OP2	11:A:812:G:N2	2.18	0.75
11:A:830:G:N2	11:A:856:C:O2	2.13	0.75
11:A:768:A:N3	11:A:1512:U:O2'	2.19	0.75
5:L:30:ARG:NH1	11:A:363:A:OP2	2.20	0.75
1:D:43:ARG:NH1	1:D:44:LYS:O	2.19	0.75
2:F:29:ILE:HG21	2:F:64:VAL:HG21	1.68	0.75
1:D:9:LYS:HG3	1:D:37:PRO:HB3	1.67	0.74
1:D:58:GLN:OE1	1:D:61:ARG:NH1	2.21	0.74
11:A:677:U:O2	11:A:714:G:N2	2.20	0.74
11:A:841:C:N4	11:A:844:G:N7	2.36	0.74
11:A:867:G:O2'	11:A:873:A:N1	2.21	0.74
11:A:14:U:N3	11:A:17:U:OP2	2.21	0.73
1:D:4:LEU:CD2	11:A:406:G:O5'	2.36	0.73
11:A:829:G:N1	11:A:857:C:N3	2.31	0.73
1:D:55:ARG:NH2	11:A:544:G:OP1	2.21	0.73
11:A:748:G:H2'	11:A:749:A:C8	2.23	0.73
11:A:517:G:N2	11:A:533:A:OP1	2.21	0.73
11:A:157:U:O2	11:A:164:G:O6	2.07	0.73
11:A:202:G:O2'	11:A:468:A:H8	1.72	0.73
11:A:1391:U:H2'	11:A:1392:G:H8	1.53	0.73
9:R:49:LYS:NZ	11:A:836:G:OP1	2.22	0.72
3:H:110:MET:HG2	3:H:114:ALA:CB	2.19	0.72
11:A:31:G:O2'	11:A:48:C:N4	2.23	0.72
1:D:94:GLU:OE2	1:D:103:ARG:NH1	2.22	0.72
11:A:789:U:OP1	11:A:794:A:N6	2.23	0.72
1:D:8:LEU:HB2	11:A:430:A:OP1	1.90	0.71
10:T:78:LEU:O	10:T:82:ILE:HG12	1.90	0.71
5:L:66:ILE:HD12	5:L:96:THR:CG2	2.20	0.71
11:A:829:G:N2	11:A:857:C:O2	2.14	0.71
1:D:33:ILE:HG22	1:D:34:GLU:N	1.98	0.71
11:A:601:G:N2	11:A:637:C:O2	2.19	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:663:A:N6	11:A:742:G:H1	1.86	0.71
1:D:8:LEU:HD23	11:A:429:U:C5'	2.20	0.70
11:A:454:G:H22	11:A:478:A:H2	1.36	0.70
11:A:1392:G:N2	11:A:1502:A:O5'	2.24	0.70
11:A:748:G:H2'	11:A:749:A:H8	1.56	0.70
6:O:53:ARG:NH1	11:A:579:A:O2'	2.21	0.70
11:A:182:A:H2	11:A:194:C:H42	1.39	0.70
1:D:30:LYS:O	1:D:31:CYS:SG	2.48	0.70
11:A:457:G:N1	11:A:475:C:N3	2.33	0.70
4:K:28:ASN:OD1	4:K:46:ALA:HB3	1.92	0.70
5:L:113:ARG:NH2	11:A:501:C:OP1	2.24	0.70
11:A:86:G:H1'	11:A:87:C:C5	2.27	0.70
11:A:94:G:N1	11:A:97:G:O6	2.24	0.70
11:A:697:U:O2'	11:A:785:G:N3	2.24	0.69
11:A:859:G:OP2	11:A:869:G:N1	2.24	0.69
1:D:58:GLN:O	1:D:62:ARG:HG2	1.92	0.69
2:F:10:VAL:O	2:F:58:HIS:N	2.25	0.69
3:H:61:THR:HG23	3:H:61:THR:O	1.91	0.69
3:H:55:LYS:NZ	11:A:652:U:O3'	2.22	0.69
10:T:8:LYS:NZ	10:T:12:GLN:OE1	2.26	0.69
1:D:9:LYS:CG	1:D:37:PRO:HB2	2.22	0.69
8:Q:47:ASP:HA	12:Q:103:HOH:O	1.91	0.69
11:A:206:C:C6	12:A:1732:HOH:O	2.45	0.69
4:K:46:ALA:HB2	4:K:65:ALA:HB2	1.74	0.69
7:P:71:VAL:O	7:P:75:ILE:HG13	1.92	0.69
11:A:736:C:H2'	11:A:737:C:C6	2.28	0.69
11:A:861:G:O6	11:A:869:G:N2	2.25	0.69
11:A:204:G:C4	11:A:465:A:H1'	2.28	0.69
11:A:509:A:N3	11:A:543:U:O2'	2.26	0.69
11:A:714:G:O2'	11:A:777:A:N6	2.26	0.68
1:D:197:HIS:HA	1:D:200:VAL:HG22	1.74	0.68
11:A:297:G:N2	11:A:300:A:OP2	2.19	0.68
11:A:744:C:H2'	11:A:745:G:C8	2.28	0.68
11:A:674:G:N2	11:A:717:U:O2	2.26	0.68
11:A:693:G:H1	11:A:788:U:H4'	1.58	0.68
4:K:62:ALA:HB1	4:K:95:THR:HB	1.75	0.68
4:K:100:ASN:ND2	4:K:104:PHE:O	2.26	0.68
11:A:837:U:O2	11:A:849:G:O6	2.12	0.68
11:A:204:G:C8	11:A:465:A:H8	2.12	0.68
1:D:56:GLU:HG2	1:D:198:LEU:HD13	1.74	0.68
11:A:465:A:H3'	11:A:465:A:N3	2.09	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:K:28:ASN:ND2	11:A:689:C:OP1	2.27	0.67
7:P:18:GLN:OE1	7:P:35:ARG:NH1	2.24	0.67
11:A:159:G:N2	11:A:162:A:OP2	2.20	0.67
11:A:1507:A:H2'	11:A:1508:A:C8	2.29	0.67
8:Q:27:PHE:CE2	8:Q:36:PHE:HB3	2.29	0.67
11:A:443:C:N3	11:A:491:G:N1	2.32	0.67
11:A:76:G:H3'	11:A:77:A:H8	1.59	0.67
11:A:578:C:O2'	11:A:728:A:N3	2.22	0.67
11:A:744:C:H2'	11:A:745:G:H8	1.56	0.67
11:A:514:C:H3'	11:A:532:A:H61	1.58	0.67
2:F:5:GLU:HA	2:F:63:ASN:HA	1.75	0.67
8:Q:30:HIS:N	8:Q:35:LYS:O	2.27	0.67
11:A:898:G:N2	11:A:901:A:OP2	2.28	0.67
11:A:1518:A:O2'	11:A:1519:A:O5'	2.13	0.67
1:D:187:ARG:O	1:D:187:ARG:NH1	2.28	0.66
11:A:443:C:O2	11:A:491:G:N2	2.16	0.66
1:D:4:LEU:HD23	11:A:406:G:O5'	1.93	0.66
11:A:522:C:H1'	11:A:536:C:H5"	1.77	0.66
2:F:12:PRO:HG3	2:F:56:LYS:HB2	1.77	0.66
11:A:441:A:H61	11:A:493:A:N6	1.93	0.66
11:A:685:G:O2'	11:A:686:U:O4'	2.13	0.66
11:A:193:C:H5	12:A:1808:HOH:O	1.77	0.66
11:A:455:G:C8	12:A:1652:HOH:O	2.48	0.66
11:A:334:C:O2'	11:A:335:C:H5'	1.95	0.65
5:L:71:HIS:CD2	5:L:73:LEU:H	2.14	0.65
11:A:8:A:O2'	11:A:559:A:OP2	2.13	0.65
5:L:66:ILE:HD11	5:L:98:ARG:HH11	1.59	0.65
11:A:11:G:HO2'	11:A:525:C:HO2'	1.41	0.65
11:A:22:G:O2'	11:A:913:A:N1	2.26	0.65
11:A:462:G:N2	11:A:470:C:O2	2.18	0.65
1:D:8:LEU:HD23	1:D:31:CYS:CB	2.26	0.65
7:P:74:LEU:CD2	12:P:107:HOH:O	2.44	0.65
4:K:80:ASN:HA	4:K:105:ARG:H	1.62	0.65
11:A:181:A:O2'	11:A:194:C:N4	2.30	0.65
11:A:714:G:O2'	11:A:715:A:O4'	2.15	0.65
11:A:15:G:OP1	11:A:1397:C:N4	2.29	0.64
11:A:674:G:H2'	11:A:675:A:C8	2.31	0.64
1:D:119:HIS:ND1	11:A:437:U:O2'	2.23	0.64
2:F:37:HIS:HB2	2:F:97:THR:HG23	1.78	0.64
11:A:839:C:N4	11:A:847:G:O6	2.30	0.64
10:T:48:LYS:O	10:T:52:GLU:HG2	1.97	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:837:U:H2'	11:A:838:G:H8	1.61	0.64
11:A:459:A:P	11:A:474:G:H22	2.21	0.64
11:A:926:G:OP2	11:A:927:G:N2	2.31	0.64
11:A:171:A:H2'	11:A:172:A:C8	2.33	0.64
7:P:74:LEU:HD21	12:P:107:HOH:O	1.98	0.64
11:A:727:G:N2	11:A:730:G:OP2	2.23	0.64
1:D:30:LYS:HE3	11:A:410:G:N7	2.12	0.63
9:R:41:SER:OG	9:R:42:ARG:NH2	2.31	0.63
11:A:204:G:C5	11:A:465:A:H1'	2.34	0.63
11:A:411:A:C6	11:A:430:A:N7	2.65	0.63
3:H:122:GLY:HA2	12:A:1774:HOH:O	1.97	0.63
1:D:25:ARG:HD3	1:D:30:LYS:CD	2.27	0.63
6:O:41:HIS:CD2	11:A:739:C:O2'	2.51	0.63
11:A:747:A:H2'	11:A:748:G:C8	2.34	0.63
1:D:68:GLU:OE1	1:D:72:ARG:NH2	2.32	0.63
11:A:407:U:H2'	11:A:408:A:C8	2.33	0.63
11:A:444:G:O6	11:A:490:C:N4	2.28	0.63
4:K:52:ARG:NH1	11:A:690:G:N7	2.44	0.63
11:A:244:U:O4	11:A:893:C:N3	2.31	0.63
5:L:53:ARG:HG3	5:L:61:GLU:OE2	1.99	0.62
1:D:25:ARG:HD3	1:D:30:LYS:HD2	1.81	0.62
5:L:66:ILE:HD11	5:L:98:ARG:NH1	2.15	0.62
11:A:632:U:H5"	11:A:633:G:C8	2.35	0.62
1:D:69:ARG:NH2	11:A:401:C:OP2	2.33	0.62
11:A:59:A:H5"	11:A:387:U:H5"	1.81	0.62
1:D:9:LYS:CD	1:D:37:PRO:HB2	2.30	0.62
2:F:42:TRP:O	2:F:45:ARG:NH1	2.27	0.62
11:A:519:C:N4	11:A:529:G:O2'	2.32	0.62
11:A:651:C:N4	11:A:753:A:OP2	2.32	0.62
11:A:84:U:H2'	11:A:86:G:H21	1.63	0.62
11:A:352:C:O2'	11:A:354:G:OP1	2.12	0.62
11:A:911:U:H2'	11:A:912:C:C6	2.35	0.62
1:D:9:LYS:HG3	1:D:37:PRO:CG	2.29	0.62
1:D:49:ASP:O	1:D:53:GLN:HG3	1.99	0.62
5:L:19:ASN:OD1	5:L:20:VAL:N	2.31	0.62
5:L:113:ARG:HG2	5:L:118:VAL:HG13	1.81	0.62
3:H:110:MET:HG2	3:H:114:ALA:HB3	1.82	0.61
11:A:675:A:H3'	11:A:676:A:H8	1.66	0.61
4:K:16:SER:HA	4:K:78:ILE:HA	1.81	0.61
11:A:343:U:O2'	11:A:346:G:O6	2.09	0.61
11:A:427:U:OP2	11:A:428:G:O2'	2.16	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:14:GLN:HG2	2:F:83:ALA:HA	1.80	0.61
4:K:33:ILE:O	4:K:41:LEU:N	2.23	0.61
4:K:51:PHE:HB2	4:K:55:ARG:HH22	1.65	0.61
5:L:106:VAL:HG23	5:L:109:ARG:HB2	1.81	0.61
6:O:64:LYS:NZ	11:A:581:G:OP1	2.33	0.61
1:D:4:LEU:HD23	11:A:406:G:C5'	2.30	0.61
1:D:75:TYR:HD1	1:D:89:LEU:CD1	2.13	0.61
6:O:22:GLY:HA3	11:A:750:C:O2	2.01	0.60
11:A:17:U:H2'	11:A:18:C:H6	1.66	0.60
11:A:204:G:C8	11:A:465:A:C8	2.89	0.60
6:O:32:THR:HB	6:O:62:ARG:HD2	1.83	0.60
11:A:411:A:N1	11:A:430:A:N7	2.48	0.60
9:R:31:TYR:HE1	9:R:44:THR:HG21	1.67	0.60
8:Q:25:GLU:OE2	8:Q:38:LYS:HB3	2.02	0.60
11:A:450:G:H5"	11:A:451:A:C5'	2.32	0.60
11:A:908:A:H2'	11:A:909:A:H8	1.67	0.60
1:D:10:LEU:HD21	1:D:62:ARG:HD2	1.83	0.60
2:F:11:HIS:O	2:F:15:SER:N	2.35	0.60
3:H:81:GLY:O	3:H:82:LEU:HD22	2.01	0.60
11:A:89:U:H2'	11:A:90:C:C6	2.37	0.59
11:A:207:C:C5	12:A:1732:HOH:O	2.37	0.59
5:L:66:ILE:HD13	5:L:73:LEU:HD11	1.83	0.59
6:O:71:ARG:NH2	11:A:754:C:O5'	2.35	0.59
8:Q:25:GLU:OE1	8:Q:40:THR:OG1	2.20	0.59
11:A:804:U:OP2	11:A:805:C:N4	2.33	0.59
11:A:842:U:O2'	11:A:843:U:OP1	2.20	0.59
11:A:740:U:H2'	11:A:741:G:C8	2.36	0.59
3:H:94:VAL:HG21	3:H:101:ALA:HB2	1.85	0.59
11:A:335:C:O2'	11:A:336:A:H8	1.75	0.59
6:O:1:SER:OG	11:A:740:U:OP1	2.21	0.59
6:O:6:ALA:HA	6:O:9:LYS:HG2	1.85	0.59
11:A:266:G:O2'	11:A:267:C:H3'	2.03	0.59
11:A:91:U:H2'	11:A:92:U:C6	2.38	0.58
11:A:919:A:H2'	11:A:920:U:C6	2.38	0.58
11:A:925:G:O2'	11:A:1503:A:N6	2.32	0.58
1:D:149:LYS:HB3	1:D:177:MET:CE	2.33	0.58
5:L:66:ILE:HA	5:L:96:THR:CG2	2.33	0.58
5:L:97:VAL:HG12	5:L:100:ALA:HB2	1.84	0.58
3:H:55:LYS:HZ1	11:A:653:U:P	2.27	0.58
4:K:58:THR:HG23	4:K:61:ALA:H	1.69	0.58
7:P:47:GLU:OE1	11:A:616:G:O2'	2.21	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:79:G:O6	11:A:90:C:N4	2.24	0.58
11:A:465:A:H3'	11:A:465:A:C4	2.39	0.58
11:A:789:U:C2	11:A:791:G:H5"	2.38	0.58
4:K:12:ARG:NH1	4:K:40:ALA:O	2.34	0.58
11:A:76:G:O6	11:A:93:U:O4	2.20	0.58
11:A:493:A:H3'	11:A:494:G:C8	2.37	0.58
3:H:38:VAL:O	3:H:42:GLU:HG3	2.03	0.58
5:L:11:ARG:NH1	11:A:563:A:N3	2.51	0.58
10:T:56:ILE:O	10:T:60:GLN:HG2	2.02	0.58
7:P:54:LEU:HD23	7:P:57:ILE:HD12	1.84	0.58
11:A:1520:C:H2'	11:A:1521:C:C6	2.38	0.58
5:L:17:LYS:NZ	11:A:885:G:O6	2.36	0.58
11:A:203:G:H1'	11:A:465:A:N7	2.18	0.58
5:L:56:LEU:HD21	5:L:81:ILE:HD11	1.86	0.58
5:L:98:ARG:HH21	5:L:106:VAL:HG12	1.67	0.58
1:D:56:GLU:CD	1:D:198:LEU:HB2	2.23	0.58
2:F:3:HIS:HB2	2:F:92:THR:HB	1.85	0.58
2:F:10:VAL:HG11	2:F:18:VAL:HG22	1.86	0.58
11:A:435:A:C8	12:A:1632:HOH:O	2.52	0.58
4:K:28:ASN:ND2	4:K:45:THR:OG1	2.35	0.58
11:A:747:A:H2'	11:A:748:G:H8	1.68	0.58
2:F:26:THR:HG22	2:F:62:MET:CE	2.34	0.57
11:A:908:A:H2'	11:A:909:A:C8	2.39	0.57
11:A:121:U:H5"	12:A:1609:HOH:O	2.02	0.57
11:A:252:U:O4	11:A:253:A:N6	2.38	0.57
11:A:462:G:P	11:A:462:G:C8	2.98	0.57
11:A:695:A:H2'	11:A:696:A:O4'	2.04	0.57
11:A:715:A:OP1	11:A:805:C:O2'	2.20	0.57
11:A:766:A:N7	11:A:813:U:O2	2.38	0.57
4:K:22:ILE:HA	4:K:31:VAL:HG22	1.85	0.57
5:L:69:GLU:HG2	11:A:521:G:H4'	1.87	0.57
11:A:487:A:H3'	11:A:488:C:H6	1.70	0.57
11:A:788:U:H3'	11:A:789:U:C6	2.40	0.57
2:F:8:PHE:HB2	2:F:84:VAL:HG11	1.85	0.57
7:P:76:LYS:HG2	7:P:80:LYS:HE3	1.87	0.57
11:A:779:C:O2'	11:A:780:A:O4'	2.20	0.57
1:D:32:LYS:O	1:D:33:ILE:HD13	2.05	0.57
8:Q:16:MET:SD	11:A:253:A:O2'	2.61	0.57
11:A:12:U:O2	11:A:22:G:O6	2.23	0.57
11:A:157:U:H1'	11:A:165:G:N2	2.20	0.57
11:A:832:G:N2	11:A:854:U:O2	2.32	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:36:ILE:HD13	2:F:62:MET:CE	2.34	0.57
5:L:58:ASN:OD1	5:L:60:PHE:HD2	1.87	0.57
10:T:2:ASN:HD21	10:T:7:LYS:HG2	1.70	0.57
1:D:112:GLU:OE1	11:A:407:U:O2'	2.23	0.56
1:D:56:GLU:HG2	1:D:198:LEU:HD12	1.87	0.56
6:O:77:TYR:O	6:O:81:ILE:HG12	2.04	0.56
11:A:79:G:H2'	11:A:80:A:C8	2.40	0.56
11:A:450:G:H5"	11:A:451:A:H5'	1.88	0.56
11:A:487:A:H3'	11:A:488:C:C6	2.41	0.56
11:A:670:G:C6	11:A:671:G:O6	2.58	0.56
11:A:767:A:O2'	11:A:1524:C:O2	2.24	0.56
11:A:693:G:N1	11:A:788:U:H4'	2.21	0.56
5:L:56:LEU:HD21	5:L:81:ILE:CD1	2.36	0.56
9:R:33:THR:HG22	9:R:37:LYS:H	1.71	0.56
11:A:721:G:H5'	11:A:722:G:C8	2.41	0.56
11:A:1501:C:OP2	11:A:1504:G:O2'	2.23	0.56
11:A:126:G:OP1	11:A:605:U:O2'	2.19	0.56
11:A:335:C:O2'	11:A:336:A:O5'	2.23	0.56
2:F:44:ARG:HG2	2:F:56:LYS:HB3	1.87	0.56
11:A:464:U:H2'	11:A:466:A:OP1	2.06	0.56
11:A:847:G:H2'	11:A:848:C:C6	2.41	0.56
9:R:36:GLY:O	9:R:62:ARG:NH2	2.39	0.56
11:A:21:G:H2'	11:A:22:G:C8	2.40	0.56
2:F:2:ARG:HD3	2:F:92:THR:HG23	1.86	0.55
9:R:22:TYR:HA	9:R:57:ALA:HB1	1.88	0.55
11:A:269:C:H2'	11:A:270:A:C8	2.42	0.55
11:A:382:A:H2'	11:A:383:A:C8	2.41	0.55
11:A:692:U:N3	11:A:695:A:OP2	2.28	0.55
11:A:1508:A:H2'	11:A:1509:C:O4'	2.06	0.55
2:F:18:VAL:HG13	2:F:22:ILE:HD11	1.88	0.55
5:L:33:CYS:H	5:L:54:VAL:HG23	1.70	0.55
3:H:39:LEU:O	3:H:43:GLY:N	2.37	0.55
5:L:98:ARG:HH21	5:L:106:VAL:CG1	2.19	0.55
6:O:4:THR:O	6:O:7:THR:OG1	2.21	0.55
6:O:32:THR:HG21	6:O:84:LEU:HD21	1.88	0.55
7:P:7:ALA:HB1	7:P:29:ASN:HB3	1.88	0.55
11:A:90:C:H2'	11:A:91:U:C6	2.41	0.55
11:A:691:G:H1'	11:A:696:A:N6	2.21	0.55
11:A:1526:G:H2'	11:A:1527:U:C6	2.41	0.55
1:D:4:LEU:HD23	11:A:406:G:H5'	1.88	0.55
1:D:171:GLU:HG3	1:D:182:LYS:HD2	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:K:12:ARG:NH1	11:A:684:U:O3'	2.39	0.55
6:O:35:ILE:HD12	6:O:62:ARG:CZ	2.36	0.55
1:D:150:LYS:HD2	1:D:150:LYS:O	2.07	0.55
3:H:12:ARG:NH1	11:A:826:C:C5'	2.69	0.55
11:A:410:G:C6	11:A:429:U:O2'	2.58	0.55
11:A:782:A:H3'	11:A:783:C:H6	1.71	0.55
11:A:362:G:N1	11:A:365:U:OP2	2.37	0.55
1:D:8:LEU:CD2	11:A:429:U:H5'	2.34	0.55
5:L:55:ARG:HB2	5:L:61:GLU:OE1	2.06	0.55
5:L:113:ARG:CG	5:L:118:VAL:HG13	2.36	0.55
11:A:740:U:H2'	11:A:741:G:H8	1.71	0.55
1:D:104:MET:HG2	1:D:170:LEU:HD13	1.89	0.55
11:A:448:A:H5"	12:A:1666:HOH:O	2.07	0.55
11:A:837:U:H2'	11:A:838:G:C8	2.41	0.55
1:D:109:THR:H	1:D:112:GLU:HB3	1.72	0.55
8:Q:8:GLN:NE2	8:Q:78:VAL:HG21	2.22	0.55
11:A:31:G:HO2'	11:A:48:C:N4	2.05	0.55
11:A:1525:G:H2'	11:A:1526:G:H8	1.70	0.55
6:O:47:LYS:CE	11:A:808:C:OP1	2.46	0.54
11:A:147:G:H2'	11:A:148:G:C8	2.42	0.54
1:D:60:VAL:HG21	1:D:199:ILE:HD11	1.89	0.54
6:O:27:GLN:O	6:O:31:LEU:HG	2.07	0.54
11:A:459:A:H2'	11:A:460:A:H8	1.72	0.54
1:D:137:SER:OG	1:D:140:ASP:OD2	2.23	0.54
2:F:38:ARG:HG2	2:F:63:ASN:HB2	1.89	0.54
7:P:14:ARG:HA	7:P:42:ILE:CD1	2.36	0.54
11:A:131:A:H2'	11:A:132:C:C6	2.42	0.54
1:D:4:LEU:HD21	11:A:406:G:O5'	2.06	0.54
11:A:70:U:O2'	11:A:94:G:N7	2.38	0.54
11:A:601:G:H2'	11:A:602:A:C8	2.43	0.54
11:A:658:C:N4	11:A:748:G:O6	2.41	0.54
11:A:768:A:H4'	11:A:1523:G:N2	2.21	0.54
8:Q:42:LYS:NZ	11:A:278:G:OP2	2.35	0.54
11:A:62:U:H2'	11:A:63:C:C6	2.43	0.54
11:A:475:C:H2'	11:A:476:U:C6	2.41	0.54
2:F:9:MET:HB2	2:F:57:ALA:HB1	1.88	0.54
11:A:11:G:O2'	11:A:525:C:O2'	2.17	0.54
8:Q:69:THR:OG1	11:A:254:G:OP1	2.24	0.54
11:A:779:C:H2'	11:A:780:A:C5	2.43	0.54
6:O:80:LEU:HA	6:O:83:ARG:HG2	1.90	0.54
11:A:462:G:P	11:A:462:G:H8	2.30	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:840:C:H2'	11:A:841:C:H5"	1.90	0.54
10:T:2:ASN:HA	11:A:332:G:OP2	2.07	0.54
11:A:737:C:H2'	11:A:738:C:H6	1.71	0.54
7:P:14:ARG:HA	7:P:42:ILE:HD13	1.90	0.54
11:A:374:A:H5"	11:A:452:A:C2	2.43	0.54
11:A:710:G:H2'	11:A:711:G:C8	2.43	0.54
1:D:33:ILE:CG2	1:D:34:GLU:H	2.00	0.53
3:H:79:ARG:HD2	11:A:878:A:OP1	2.09	0.53
1:D:97:LEU:HA	1:D:100:VAL:HG12	1.89	0.53
4:K:33:ILE:HD12	4:K:81:LEU:HD13	1.89	0.53
6:O:32:THR:HB	6:O:86:LEU:HD11	1.89	0.53
10:T:58:ASP:OD2	11:A:194:C:O4'	2.25	0.53
10:T:43:LYS:HD3	10:T:86:ALA:HA	1.91	0.53
11:A:251:G:C6	11:A:266:G:C2	2.96	0.53
4:K:52:ARG:HB3	11:A:691:G:O6	2.08	0.53
5:L:18:SER:HB3	5:L:21:PRO:HB3	1.90	0.53
11:A:779:C:H2'	11:A:780:A:C4	2.44	0.53
11:A:1525:G:H2'	11:A:1526:G:C8	2.43	0.53
1:D:4:LEU:CD2	11:A:406:G:C5'	2.86	0.53
11:A:266:G:O2'	11:A:267:C:O5'	2.25	0.53
11:A:730:G:O2'	11:A:814:A:N6	2.42	0.53
11:A:735:C:H2'	11:A:736:C:C6	2.44	0.53
11:A:838:G:H2'	11:A:839:C:H6	1.73	0.53
1:D:33:ILE:HB	1:D:34:GLU:OE1	2.08	0.53
2:F:46:GLN:HE22	2:F:56:LYS:HG3	1.74	0.53
3:H:1:SER:H2	3:H:5:PRO:HA	1.74	0.53
3:H:42:GLU:OE2	3:H:44:PHE:CD2	2.46	0.53
4:K:32:THR:HB	11:A:705:G:H22	1.73	0.53
11:A:18:C:H2'	11:A:19:A:O4'	2.09	0.53
11:A:665:A:H2'	11:A:732:C:O2	2.09	0.53
3:H:12:ARG:HH12	11:A:826:C:H5"	1.74	0.53
6:O:47:LYS:HE2	11:A:808:C:P	2.49	0.52
11:A:500:G:H2'	11:A:501:C:C6	2.44	0.52
11:A:843:U:H4'	11:A:844:G:OP1	2.09	0.52
8:Q:57:VAL:O	8:Q:78:VAL:HG22	2.09	0.52
11:A:371:A:H2'	11:A:372:C:O4'	2.08	0.52
11:A:575:G:H4'	11:A:576:C:H5"	1.91	0.52
11:A:592:G:C6	11:A:648:A:C6	2.97	0.52
11:A:658:C:C2	11:A:748:G:N2	2.77	0.52
11:A:681:A:N6	11:A:682:G:O6	2.41	0.52
11:A:734:G:H2'	11:A:735:C:C6	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:783:C:H2'	11:A:784:A:C8	2.44	0.52
11:A:925:G:H1'	11:A:1392:G:O6	2.08	0.52
2:F:4:TYR:CD2	2:F:66:ALA:HB3	2.44	0.52
11:A:204:G:C4	11:A:205:A:C8	2.98	0.52
11:A:832:G:H2'	11:A:833:G:C8	2.45	0.52
5:L:71:HIS:HD2	5:L:73:LEU:H	1.54	0.52
9:R:49:LYS:HA	9:R:52:ARG:HE	1.73	0.52
6:O:45:HIS:C	6:O:47:LYS:H	2.13	0.52
10:T:77:ASN:O	10:T:81:GLN:HG2	2.10	0.52
11:A:691:G:N2	11:A:696:A:C8	2.78	0.52
11:A:212:G:C4	11:A:213:G:C8	2.97	0.52
11:A:516:U:H3'	11:A:517:G:C8	2.45	0.52
6:O:76:ARG:HG2	6:O:79:ARG:HH22	1.75	0.52
11:A:91:U:H2'	11:A:92:U:H6	1.75	0.52
11:A:411:A:N1	11:A:430:A:C6	2.76	0.52
11:A:710:G:H2'	11:A:711:G:H8	1.74	0.52
3:H:47:ASP:H	3:H:61:THR:CG2	2.23	0.52
7:P:4:ILE:HD12	7:P:21:VAL:HG22	1.92	0.52
7:P:5:ARG:NH2	7:P:24:SER:O	2.43	0.52
11:A:77:A:H2'	11:A:78:A:O4'	2.10	0.52
11:A:82:G:N2	11:A:84:U:O4	2.43	0.52
11:A:134:G:H1'	11:A:325:A:C5	2.45	0.52
11:A:182:A:H1'	11:A:183:C:C5	2.45	0.52
11:A:859:G:H2'	11:A:860:A:C8	2.45	0.52
11:A:118:U:H3'	11:A:288:A:H61	1.75	0.51
11:A:893:C:H2'	11:A:894:G:C8	2.45	0.51
11:A:920:U:H2'	11:A:921:U:C5	2.45	0.51
11:A:1393:U:H3'	11:A:1394:A:C8	2.45	0.51
1:D:75:TYR:CD1	1:D:89:LEU:HD12	2.45	0.51
2:F:29:ILE:HD13	2:F:64:VAL:HG11	1.93	0.51
8:Q:13:SER:HA	8:Q:54:ILE:CD1	2.40	0.51
11:A:1394:A:H2'	11:A:1395:C:O4'	2.10	0.51
2:F:37:HIS:ND1	2:F:65:GLU:HG3	2.25	0.51
5:L:97:VAL:CG1	5:L:100:ALA:HB2	2.40	0.51
9:R:42:ARG:NH1	11:A:721:G:OP2	2.42	0.51
11:A:150:U:H2'	11:A:151:A:C8	2.46	0.51
11:A:737:C:H2'	11:A:738:C:C6	2.46	0.51
5:L:66:ILE:HA	5:L:96:THR:HG22	1.92	0.51
9:R:62:ARG:NH2	11:A:719:C:O2	2.38	0.51
11:A:658:C:H2'	11:A:659:U:H6	1.75	0.51
11:A:770:C:H2'	11:A:771:G:C8	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:785:G:H8	11:A:785:G:P	2.34	0.51
2:F:38:ARG:NH1	2:F:98:GLU:O	2.44	0.51
3:H:61:THR:O	3:H:61:THR:CG2	2.58	0.51
11:A:675:A:H3'	11:A:676:A:C8	2.44	0.51
3:H:21:LYS:O	3:H:64:TYR:OH	2.27	0.51
9:R:60:ARG:O	9:R:64:LEU:N	2.44	0.51
9:R:63:TYR:OH	11:A:734:G:N3	2.39	0.51
10:T:61:ALA:HA	10:T:66:ILE:O	2.11	0.51
11:A:465:A:H4'	11:A:466:A:N6	2.25	0.51
11:A:481:G:O2'	11:A:483:C:N4	2.40	0.51
11:A:770:C:H2'	11:A:771:G:H8	1.76	0.51
1:D:87:GLU:OE1	1:D:187:ARG:HB2	2.11	0.51
11:A:207:C:H2'	11:A:208:U:O4'	2.11	0.51
4:K:32:THR:HB	11:A:705:G:N2	2.26	0.51
7:P:52:LEU:HD12	7:P:78:VAL:HG21	1.93	0.51
11:A:580:C:H2'	11:A:581:G:O4'	2.10	0.51
1:D:151:GLN:HE22	1:D:153:ARG:HE	1.59	0.51
2:F:44:ARG:HA	2:F:58:HIS:HA	1.93	0.51
2:F:86:ARG:HG2	2:F:88:MET:SD	2.51	0.51
3:H:39:LEU:HD21	3:H:128:VAL:HG21	1.92	0.50
4:K:105:ARG:NH1	4:K:106:ILE:O	2.43	0.50
7:P:40:ASN:HB3	7:P:43:ALA:HB2	1.93	0.50
11:A:468:A:H5'	11:A:469:C:OP2	2.11	0.50
11:A:728:A:H2'	11:A:729:A:C8	2.46	0.50
1:D:75:TYR:HD1	1:D:89:LEU:HD12	1.74	0.50
3:H:10:LEU:HD22	3:H:74:ILE:HD11	1.93	0.50
9:R:48:ALA:O	9:R:52:ARG:NE	2.44	0.50
1:D:1:ALA:HB2	11:A:547:A:OP2	2.09	0.50
1:D:13:ARG:HH11	1:D:37:PRO:HD2	1.77	0.50
3:H:47:ASP:H	3:H:61:THR:HG22	1.75	0.50
11:A:251:G:C4	11:A:266:G:C5	2.99	0.50
11:A:413:G:H4'	11:A:414:A:H5"	1.93	0.50
11:A:836:G:O6	11:A:850:U:O4	2.29	0.50
2:F:36:ILE:HG21	2:F:62:MET:HE3	1.94	0.50
4:K:48:GLY:N	4:K:52:ARG:HD3	2.26	0.50
5:L:22:ALA:HB3	5:L:94:TYR:OH	2.11	0.50
11:A:722:G:H1	11:A:733:G:H1	1.59	0.50
1:D:75:TYR:OH	1:D:200:VAL:HA	2.11	0.50
8:Q:19:SER:HB3	8:Q:70:LYS:NZ	2.26	0.50
11:A:429:U:H1'	11:A:430:A:H5"	1.94	0.50
11:A:625:U:H2'	11:A:626:G:C8	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:785:G:H2'	11:A:786:G:C8	2.47	0.50
5:L:46:SER:HB3	11:A:519:C:OP2	2.11	0.50
11:A:157:U:O2	11:A:164:G:C6	2.64	0.50
11:A:381:C:H2'	11:A:382:A:O4'	2.12	0.50
11:A:863:U:O2'	11:A:865:A:N7	2.35	0.50
11:A:1393:U:H3'	11:A:1394:A:H8	1.77	0.50
1:D:9:LYS:CG	1:D:37:PRO:CB	2.71	0.50
1:D:12:ARG:NH2	11:A:427:U:OP1	2.45	0.50
3:H:55:LYS:O	3:H:57:GLU:OE1	2.30	0.50
8:Q:27:PHE:CZ	8:Q:36:PHE:CB	2.95	0.50
2:F:26:THR:HG22	2:F:62:MET:HE2	1.92	0.49
11:A:251:G:C4	11:A:266:G:C6	3.00	0.49
11:A:1513:A:H2'	11:A:1514:G:H8	1.77	0.49
1:D:2:ARG:NH2	11:A:406:G:O3'	2.40	0.49
3:H:103:VAL:HG23	3:H:105:THR:HG23	1.94	0.49
6:O:32:THR:CB	6:O:86:LEU:HD11	2.43	0.49
9:R:46:THR:O	9:R:46:THR:HG22	2.12	0.49
11:A:1520:C:H2'	11:A:1521:C:H6	1.75	0.49
1:D:49:ASP:OD1	1:D:50:TYR:N	2.45	0.49
3:H:2:MET:HE1	11:A:756:C:O4'	2.11	0.49
1:D:109:THR:HG23	1:D:112:GLU:H	1.77	0.49
1:D:160:LEU:HA	1:D:163:GLN:OE1	2.12	0.49
8:Q:15:LYS:HE2	11:A:275:G:H5'	1.94	0.49
10:T:27:MET:HG3	10:T:57:VAL:HG12	1.94	0.49
11:A:218:U:H2'	11:A:219:U:O4'	2.11	0.49
11:A:695:A:H61	11:A:786:G:N2	2.02	0.49
2:F:5:GLU:OE1	9:R:22:TYR:OH	2.29	0.49
3:H:115:ALA:O	3:H:119:GLY:N	2.43	0.49
10:T:28:ARG:HG3	10:T:28:ARG:HH11	1.78	0.49
11:A:916:U:H2'	11:A:917:G:H8	1.77	0.49
1:D:106:PHE:CD1	1:D:144:ILE:HD11	2.48	0.49
6:O:32:THR:HB	6:O:62:ARG:CD	2.42	0.49
11:A:711:G:H2'	11:A:712:A:C8	2.47	0.49
1:D:149:LYS:CB	1:D:177:MET:CE	2.90	0.49
5:L:55:ARG:HG2	5:L:55:ARG:HH11	1.78	0.49
7:P:35:ARG:HD3	12:A:1924:HOH:O	2.12	0.49
11:A:714:G:H21	11:A:777:A:H1'	1.78	0.49
6:O:34:GLN:O	6:O:38:LEU:HD13	2.13	0.49
6:O:35:ILE:HD12	6:O:62:ARG:NH1	2.28	0.49
6:O:38:LEU:CD2	6:O:55:LEU:CB	2.89	0.49
11:A:505:G:H2'	11:A:506:G:C8	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:517:G:O2'	11:A:530:G:H4'	2.13	0.49
11:A:713:G:O2'	11:A:714:G:O4'	2.13	0.49
1:D:8:LEU:CD2	11:A:429:U:C3'	2.66	0.49
3:H:14:ARG:NH2	3:H:74:ILE:O	2.43	0.49
1:D:104:MET:O	1:D:172:VAL:HG21	2.13	0.49
7:P:4:ILE:CD1	7:P:21:VAL:HG22	2.42	0.49
2:F:4:TYR:HE1	2:F:91:ARG:HD3	1.76	0.48
10:T:3:ILE:N	11:A:332:G:OP2	2.38	0.48
11:A:76:G:H3'	11:A:77:A:C8	2.45	0.48
11:A:320:A:H2'	11:A:321:A:O4'	2.13	0.48
11:A:720:C:OP2	11:A:721:G:O2'	2.30	0.48
11:A:735:C:H2'	11:A:736:C:H6	1.78	0.48
11:A:745:G:H2'	11:A:746:A:H8	1.78	0.48
11:A:768:A:H5'	11:A:1524:C:H1'	1.94	0.48
11:A:883:C:O2'	11:A:884:U:H5'	2.13	0.48
5:L:34:THR:O	5:L:75:GLU:OE1	2.31	0.48
11:A:193:C:H2'	11:A:194:C:C6	2.49	0.48
11:A:568:G:O2'	11:A:574:A:N1	2.31	0.48
11:A:712:A:H3'	11:A:713:G:C5	2.48	0.48
11:A:820:U:H4'	11:A:821:G:OP2	2.13	0.48
11:A:838:G:H2'	11:A:839:C:C6	2.47	0.48
11:A:863:U:H2'	11:A:865:A:OP2	2.13	0.48
11:A:911:U:H2'	11:A:912:C:H6	1.78	0.48
11:A:235:C:H2'	11:A:236:A:C8	2.48	0.48
11:A:236:A:H2'	11:A:237:G:C8	2.48	0.48
11:A:355:C:H2'	11:A:356:A:O4'	2.14	0.48
11:A:652:U:O4	11:A:752:G:O2'	2.23	0.48
11:A:845:A:H2'	11:A:846:G:H5'	1.95	0.48
4:K:80:ASN:HB3	4:K:105:ARG:HE	1.78	0.48
5:L:75:GLU:OE2	5:L:76:HIS:CE1	2.66	0.48
11:A:464:U:HO2'	11:A:465:A:H2	1.59	0.48
11:A:670:G:C6	11:A:671:G:C6	3.02	0.48
11:A:840:C:N3	11:A:847:G:N1	2.61	0.48
11:A:1521:C:H2'	11:A:1522:U:C6	2.48	0.48
2:F:7:VAL:HG22	2:F:61:LEU:HB2	1.96	0.48
3:H:94:VAL:CG2	3:H:101:ALA:HB2	2.43	0.48
4:K:12:ARG:NH1	11:A:684:U:O2'	2.47	0.48
4:K:66:ALA:HB3	4:K:98:ALA:HB3	1.94	0.48
5:L:22:ALA:HB3	5:L:94:TYR:CZ	2.49	0.48
9:R:38:ILE:HD12	11:A:720:C:H1'	1.95	0.48
10:T:23:ARG:NH2	11:A:176:C:H5"	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:67:C:H2'	11:A:68:G:C8	2.49	0.48
11:A:184:G:H2'	11:A:185:U:C6	2.49	0.48
11:A:204:G:H2'	11:A:205:A:O4'	2.13	0.48
11:A:284:C:H2'	11:A:285:C:C6	2.49	0.48
11:A:665:A:N7	11:A:724:G:C6	2.82	0.48
1:D:1:ALA:HB2	11:A:547:A:O5'	2.14	0.48
2:F:20:GLY:O	2:F:24:ARG:CG	2.49	0.48
11:A:450:G:H5"	11:A:451:A:H5"	1.95	0.48
11:A:502:A:H2'	11:A:503:C:O4'	2.14	0.48
11:A:854:U:H2'	11:A:855:U:H6	1.78	0.48
6:O:35:ILE:O	6:O:39:GLN:HG2	2.14	0.48
11:A:361:G:H2'	11:A:362:G:O4'	2.14	0.48
11:A:539:A:H2'	11:A:540:G:C8	2.48	0.48
11:A:678:U:H3	11:A:713:G:H22	1.61	0.48
11:A:778:G:H2'	11:A:779:C:C6	2.49	0.48
3:H:110:MET:HG2	3:H:114:ALA:HB1	1.95	0.48
11:A:431:A:H2'	11:A:432:A:O4'	2.14	0.48
11:A:458:U:H2'	11:A:474:G:C2	2.49	0.48
6:O:35:ILE:HD11	6:O:59:VAL:HA	1.95	0.47
8:Q:6:THR:HA	8:Q:60:ILE:O	2.14	0.47
11:A:417:G:H2'	11:A:418:C:C6	2.48	0.47
11:A:829:G:C6	11:A:858:G:C2	3.01	0.47
3:H:12:ARG:HH12	11:A:826:C:C5'	2.26	0.47
3:H:17:GLN:HG2	3:H:62:LEU:HD13	1.96	0.47
11:A:114:U:H1'	11:A:353:A:H1'	1.95	0.47
11:A:121:U:C5'	12:A:1609:HOH:O	2.60	0.47
11:A:206:C:H2'	11:A:207:C:H6	1.79	0.47
11:A:303:A:H2'	11:A:304:U:O4'	2.14	0.47
2:F:3:HIS:HA	2:F:65:GLU:HG2	1.95	0.47
3:H:31:LEU:O	3:H:35:ILE:HD12	2.13	0.47
4:K:31:VAL:HB	4:K:69:CYS:SG	2.54	0.47
11:A:830:G:H2'	11:A:831:A:C8	2.49	0.47
2:F:26:THR:CG2	2:F:62:MET:HE1	2.45	0.47
5:L:66:ILE:HA	5:L:96:THR:HG21	1.96	0.47
7:P:67:ILE:HG22	7:P:71:VAL:HB	1.94	0.47
1:D:16:THR:OG1	1:D:17:ASP:N	2.48	0.47
1:D:100:VAL:HG11	1:D:136:VAL:HG21	1.95	0.47
4:K:70:ALA:O	4:K:74:LYS:HG2	2.14	0.47
8:Q:59:GLU:OE2	8:Q:76:ARG:NH2	2.48	0.47
11:A:419:C:H5	12:A:1701:HOH:O	1.97	0.47
11:A:666:G:O4'	11:A:726:C:O2'	2.32	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:60:VAL:HG22	1:D:194:ILE:HD12	1.96	0.47
2:F:38:ARG:HH22	2:F:96:VAL:HG12	1.78	0.47
11:A:206:C:C5	12:A:1732:HOH:O	2.66	0.47
11:A:213:G:C8	11:A:214:C:C5	3.02	0.47
11:A:486:U:H2'	11:A:487:A:C8	2.49	0.47
3:H:57:GLU:OE1	3:H:57:GLU:N	2.48	0.47
4:K:21:HIS:HB3	4:K:32:THR:HG22	1.96	0.47
5:L:87:LYS:HE3	11:A:523:A:H2	1.80	0.47
7:P:8:ARG:HH21	7:P:15:PRO:HG3	1.80	0.47
11:A:685:G:N2	11:A:706:A:N6	2.63	0.47
11:A:713:G:H2'	11:A:714:G:C4	2.50	0.47
11:A:789:U:N3	11:A:792:A:OP2	2.29	0.47
3:H:1:SER:N	3:H:8:ASP:HB2	2.30	0.47
8:Q:67:SER:OG	8:Q:70:LYS:HB3	2.14	0.47
11:A:76:G:C6	11:A:77:A:C6	3.03	0.47
11:A:714:G:HO2'	11:A:715:A:C1'	2.27	0.47
11:A:920:U:H2'	11:A:921:U:C6	2.49	0.47
11:A:1523:G:H2'	11:A:1523:G:N3	2.30	0.47
2:F:18:VAL:HB	2:F:19:PRO:HD3	1.97	0.47
4:K:45:THR:HG21	11:A:688:G:O3'	2.15	0.47
9:R:62:ARG:HA	9:R:67:LEU:O	2.15	0.47
11:A:9:G:H2'	11:A:10:A:H8	1.80	0.47
11:A:493:A:H5'	11:A:494:G:OP2	2.15	0.47
3:H:5:PRO:O	3:H:8:ASP:HB3	2.15	0.47
9:R:42:ARG:HH22	11:A:721:G:P	2.38	0.47
11:A:864:A:H2'	11:A:865:A:C8	2.50	0.47
11:A:1502:A:C5	11:A:1530:G:H4'	2.50	0.47
2:F:4:TYR:HA	2:F:90:MET:O	2.15	0.46
3:H:12:ARG:NH1	11:A:826:C:H5'	2.30	0.46
4:K:12:ARG:HH12	11:A:684:U:HO2'	1.63	0.46
11:A:88:U:HO2'	11:A:89:U:H6	1.59	0.46
11:A:475:C:H2'	11:A:476:U:H6	1.80	0.46
11:A:582:C:N3	11:A:759:A:N7	2.63	0.46
11:A:676:A:H2	11:A:715:A:N1	2.12	0.46
11:A:923:A:C5	11:A:924:C:H5	2.32	0.46
3:H:42:GLU:CD	3:H:44:PHE:HD2	2.18	0.46
5:L:51:VAL:HG22	5:L:65:TYR:HD1	1.80	0.46
11:A:24:U:O2'	11:A:524:G:O2'	2.12	0.46
11:A:107:G:C2	11:A:108:G:H1'	2.50	0.46
11:A:649:A:H2'	11:A:650:G:O4'	2.16	0.46
2:F:68:GLN:HG2	11:A:739:C:OP1	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:O:35:ILE:CD1	6:O:59:VAL:HA	2.45	0.46
11:A:15:G:N7	11:A:1396:A:N6	2.63	0.46
11:A:38:G:H22	11:A:397:A:H5'	1.80	0.46
11:A:90:C:H2'	11:A:91:U:H6	1.80	0.46
11:A:604:G:H2'	11:A:605:U:O4'	2.15	0.46
11:A:774:G:H3'	11:A:775:G:H8	1.80	0.46
1:D:149:LYS:HB3	1:D:177:MET:HE1	1.97	0.46
1:D:171:GLU:CG	1:D:182:LYS:HD2	2.44	0.46
9:R:61:ALA:HA	9:R:64:LEU:HB3	1.95	0.46
11:A:334:C:HO2'	11:A:335:C:H5'	1.78	0.46
11:A:766:A:H2	11:A:1525:G:N3	2.13	0.46
11:A:784:A:H2'	11:A:784:A:N3	2.30	0.46
11:A:893:C:H2'	11:A:894:G:H8	1.79	0.46
11:A:98:A:H2'	11:A:99:C:C6	2.51	0.46
11:A:465:A:N6	11:A:468:A:C8	2.83	0.46
11:A:658:C:H2'	11:A:659:U:C6	2.50	0.46
11:A:1518:A:H4'	11:A:1519:A:OP1	2.15	0.46
11:A:13:U:O2	11:A:915:A:N7	2.48	0.46
11:A:93:U:H2'	11:A:95:C:C5	2.51	0.46
11:A:713:G:C4	11:A:714:G:N1	2.84	0.46
5:L:49:ARG:NH2	11:A:521:G:O6	2.49	0.46
11:A:154:U:O4	11:A:155:A:N6	2.49	0.46
11:A:301:G:H2'	11:A:302:G:C8	2.50	0.46
11:A:505:G:C2	11:A:506:G:C5	3.04	0.46
11:A:767:A:H2'	11:A:768:A:O4'	2.14	0.46
1:D:171:GLU:CD	1:D:182:LYS:HD2	2.35	0.46
9:R:19:GLU:OE1	9:R:50:TYR:OH	2.34	0.46
3:H:58:LEU:HD23	3:H:60:LEU:HB2	1.98	0.46
11:A:313:A:H2'	11:A:314:C:C6	2.50	0.46
11:A:904:U:C2	11:A:905:U:C5	3.04	0.46
8:Q:29:LYS:HA	8:Q:36:PHE:HA	1.97	0.46
11:A:206:C:H2'	11:A:207:C:C6	2.50	0.46
11:A:601:G:H2'	11:A:602:A:H8	1.80	0.46
11:A:801:U:C2	11:A:802:A:C8	3.04	0.46
2:F:18:VAL:CG1	2:F:22:ILE:HD11	2.46	0.45
11:A:123:U:H2'	11:A:124:C:C6	2.51	0.45
11:A:268:U:H2'	11:A:269:C:C6	2.51	0.45
11:A:673:A:C4	11:A:734:G:N2	2.84	0.45
11:A:836:G:C5	11:A:851:G:C6	3.04	0.45
11:A:838:G:C4	11:A:849:G:C2	3.04	0.45
11:A:839:C:H2'	11:A:840:C:C6	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:844:G:H2'	11:A:845:A:O4'	2.16	0.45
1:D:25:ARG:HD3	1:D:30:LYS:HD3	1.99	0.45
5:L:71:HIS:CD2	5:L:72:ASN:N	2.84	0.45
11:A:204:G:H2'	11:A:205:A:C8	2.51	0.45
11:A:435:A:N7	12:A:1632:HOH:O	2.47	0.45
10:T:27:MET:CG	10:T:57:VAL:HG12	2.47	0.45
11:A:239:U:H5"	11:A:240:G:OP2	2.17	0.45
11:A:787:A:H2'	11:A:788:U:C6	2.51	0.45
11:A:1390:U:H2'	11:A:1391:U:C6	2.51	0.45
11:A:1392:G:H2'	11:A:1393:U:C6	2.51	0.45
11:A:1393:U:H2'	11:A:1394:A:O4'	2.16	0.45
5:L:47:ALA:HB2	11:A:529:G:H22	1.81	0.45
11:A:212:G:C2	11:A:213:G:C8	3.04	0.45
6:O:41:HIS:CE1	6:O:44:GLU:OE1	2.68	0.45
11:A:407:U:H2'	11:A:408:A:H8	1.76	0.45
11:A:825:A:H1'	12:A:1604:HOH:O	2.17	0.45
11:A:845:A:C8	11:A:846:G:H8	2.35	0.45
11:A:1510:C:N3	11:A:1526:G:N1	2.64	0.45
6:O:35:ILE:HD13	6:O:59:VAL:HG22	1.97	0.45
8:Q:18:LYS:HD3	8:Q:48:GLU:OE2	2.16	0.45
11:A:150:U:H2'	11:A:151:A:H8	1.82	0.45
8:Q:66:LEU:HB2	8:Q:70:LYS:HG2	1.99	0.45
10:T:78:LEU:HD23	10:T:78:LEU:HA	1.67	0.45
11:A:216:U:H2'	11:A:217:C:C6	2.52	0.45
11:A:266:G:HO2'	11:A:267:C:H3'	1.82	0.45
1:D:75:TYR:CE1	1:D:200:VAL:HA	2.52	0.45
5:L:82:ARG:NH1	5:L:95:HIS:CB	2.80	0.45
11:A:266:G:O2'	11:A:268:U:OP2	2.33	0.45
11:A:459:A:OP2	11:A:474:G:N1	2.34	0.45
11:A:472:U:H2'	11:A:473:U:C6	2.52	0.45
11:A:162:A:O5'	11:A:162:A:H8	1.99	0.45
11:A:173:U:H6	11:A:198:G:HO2'	1.61	0.45
11:A:655:A:H2'	11:A:656:G:O4'	2.17	0.45
11:A:669:G:H2'	11:A:670:G:C8	2.52	0.45
11:A:679:C:N3	11:A:712:A:N1	2.65	0.45
11:A:721:G:C6	11:A:733:G:C2	3.05	0.45
11:A:746:A:C6	11:A:747:A:C6	3.05	0.45
11:A:806:C:H2'	11:A:807:A:C8	2.52	0.45
4:K:51:PHE:HE2	4:K:56:LYS:HG3	1.80	0.45
8:Q:18:LYS:HE3	11:A:255:G:O3'	2.17	0.45
11:A:678:U:H2'	11:A:679:C:C6	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:687:A:N3	11:A:688:G:H1'	2.31	0.45
2:F:12:PRO:HB3	2:F:44:ARG:HD3	1.98	0.44
4:K:22:ILE:HG22	4:K:24:ALA:HB2	1.99	0.44
11:A:33:A:H2'	11:A:34:C:C6	2.52	0.44
11:A:151:A:OP2	11:A:169:C:N4	2.49	0.44
11:A:383:A:C5	11:A:384:G:H1'	2.52	0.44
11:A:486:U:H2'	11:A:487:A:H8	1.81	0.44
11:A:518:C:H2'	11:A:530:G:C8	2.52	0.44
11:A:773:G:O6	11:A:807:A:N6	2.50	0.44
6:O:82:GLU:N	6:O:82:GLU:OE1	2.50	0.44
7:P:44:SER:OG	7:P:47:GLU:HB2	2.17	0.44
11:A:151:A:H2'	11:A:152:A:O4'	2.17	0.44
11:A:618:C:O2	11:A:622:A:N6	2.50	0.44
11:A:766:A:N7	11:A:813:U:C2	2.85	0.44
11:A:832:G:H1	11:A:854:U:H3	1.65	0.44
11:A:916:U:H2'	11:A:917:G:C8	2.52	0.44
5:L:78:VAL:O	5:L:102:ASP:HB2	2.17	0.44
11:A:1391:U:H2'	11:A:1392:G:C8	2.43	0.44
3:H:58:LEU:CD2	3:H:60:LEU:HB2	2.47	0.44
8:Q:16:MET:HG2	11:A:275:G:O2'	2.17	0.44
9:R:24:ASP:N	9:R:24:ASP:OD1	2.48	0.44
11:A:121:U:O2'	11:A:121:U:O2	2.34	0.44
11:A:309:A:O2'	11:A:607:A:N1	2.42	0.44
11:A:356:A:N3	11:A:368:U:O2'	2.46	0.44
11:A:514:C:H3'	11:A:532:A:N6	2.29	0.44
5:L:82:ARG:NH1	5:L:95:HIS:HB2	2.33	0.44
8:Q:45:VAL:HG21	8:Q:60:ILE:HG21	2.00	0.44
11:A:51:A:N7	11:A:114:U:O2'	2.49	0.44
11:A:189:A:H2'	11:A:190:A:C8	2.53	0.44
11:A:359:G:H2'	11:A:360:G:O4'	2.17	0.44
2:F:2:ARG:CD	2:F:92:THR:CG2	2.96	0.44
4:K:26:PHE:HA	4:K:90:PRO:HD3	1.99	0.44
11:A:416:G:H2'	11:A:417:G:H8	1.83	0.44
11:A:465:A:O3'	11:A:466:A:C5	2.71	0.44
1:D:1:ALA:HB2	11:A:547:A:P	2.57	0.44
6:O:48:ASP:CG	6:O:51:SER:OG	2.57	0.44
11:A:31:G:N7	11:A:306:A:H1'	2.32	0.44
11:A:50:A:N1	11:A:360:G:O2'	2.46	0.44
11:A:109:A:H2'	11:A:326:G:N2	2.33	0.44
11:A:148:G:H2'	11:A:149:A:O4'	2.18	0.44
11:A:152:A:H3'	11:A:153:C:H6	1.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:661:G:N1	11:A:745:G:C6	2.86	0.44
11:A:801:U:H2'	11:A:802:A:H8	1.83	0.44
11:A:837:U:C2	11:A:849:G:O6	2.70	0.44
1:D:30:LYS:HE3	11:A:410:G:C8	2.53	0.44
1:D:94:GLU:HA	1:D:99:ASN:ND2	2.32	0.44
1:D:112:GLU:OE2	1:D:153:ARG:CD	2.50	0.44
2:F:17:GLN:OE1	2:F:20:GLY:HA3	2.18	0.44
11:A:48:C:H6	11:A:365:U:O4	2.01	0.44
11:A:582:C:H41	11:A:758:C:H2'	1.83	0.44
11:A:843:U:H2'	11:A:844:G:C5	2.52	0.44
1:D:10:LEU:HD11	1:D:62:ARG:HD2	1.99	0.43
1:D:149:LYS:CG	1:D:177:MET:HE3	2.48	0.43
2:F:11:HIS:HB3	2:F:54:LEU:HD23	1.98	0.43
8:Q:19:SER:HB3	8:Q:70:LYS:HZ1	1.83	0.43
11:A:448:A:N7	11:A:486:U:C2	2.85	0.43
11:A:691:G:H2'	11:A:692:U:C6	2.52	0.43
11:A:696:A:H2'	11:A:697:U:O4'	2.18	0.43
11:A:1526:G:C2	11:A:1527:U:C4	3.06	0.43
4:K:16:SER:O	4:K:16:SER:OG	2.35	0.43
4:K:21:HIS:ND1	11:A:706:A:O2'	2.51	0.43
9:R:62:ARG:NH1	11:A:719:C:N3	2.48	0.43
10:T:53:MET:O	10:T:53:MET:HG2	2.16	0.43
11:A:680:C:H2'	11:A:681:A:H8	1.83	0.43
11:A:748:G:C2	11:A:749:A:C5	3.06	0.43
2:F:61:LEU:HG	2:F:63:ASN:HD21	1.82	0.43
2:F:91:ARG:HH21	11:A:738:C:P	2.41	0.43
7:P:52:LEU:HD23	7:P:52:LEU:HA	1.75	0.43
11:A:739:C:H2'	11:A:740:U:C6	2.53	0.43
4:K:80:ASN:HB3	4:K:105:ARG:NE	2.34	0.43
5:L:32:VAL:HG12	5:L:32:VAL:O	2.18	0.43
5:L:75:GLU:OE2	5:L:76:HIS:ND1	2.51	0.43
6:O:23:SER:HB2	6:O:26:VAL:HG23	2.00	0.43
6:O:32:THR:HA	6:O:62:ARG:HH11	1.82	0.43
11:A:769:G:H4'	11:A:1513:A:C4'	2.42	0.43
11:A:1395:C:H2'	11:A:1396:A:C8	2.54	0.43
2:F:43:GLY:HA2	2:F:58:HIS:CE1	2.53	0.43
6:O:66:LEU:HD13	6:O:87:ARG:HG2	1.99	0.43
11:A:15:G:H2'	11:A:16:A:O4'	2.18	0.43
11:A:56:U:H2'	11:A:57:G:C8	2.54	0.43
11:A:350:G:H2'	11:A:351:G:C8	2.54	0.43
11:A:602:A:H2'	11:A:603:U:C6	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:830:G:H2'	11:A:831:A:H8	1.84	0.43
1:D:44:LYS:NZ	1:D:46:ARG:HB2	2.33	0.43
8:Q:68:LYS:O	11:A:254:G:OP1	2.36	0.43
11:A:613:C:H2'	11:A:614:C:C6	2.54	0.43
11:A:845:A:C8	11:A:846:G:C8	3.06	0.43
2:F:18:VAL:O	2:F:22:ILE:CG1	2.58	0.43
6:O:34:GLN:O	6:O:38:LEU:CD1	2.66	0.43
11:A:270:A:H2'	11:A:271:C:C6	2.54	0.43
11:A:325:A:H2'	11:A:326:G:O4'	2.18	0.43
11:A:455:G:N7	12:A:1652:HOH:O	2.52	0.43
11:A:494:G:O2'	11:A:496:A:H1'	2.19	0.43
11:A:778:G:C6	11:A:779:C:C4	3.07	0.43
11:A:854:U:H2'	11:A:855:U:C6	2.54	0.43
5:L:2:THR:HG21	11:A:880:C:OP2	2.18	0.43
11:A:37:U:O2'	11:A:500:G:H4'	2.19	0.43
11:A:505:G:H2'	11:A:506:G:H8	1.84	0.43
11:A:608:A:H2'	11:A:609:A:O4'	2.18	0.43
11:A:768:A:H4'	11:A:1523:G:H22	1.83	0.43
1:D:8:LEU:CD2	11:A:429:U:C5'	2.94	0.43
1:D:36:ALA:HB3	1:D:41:GLY:HA2	2.01	0.43
5:L:66:ILE:CD1	5:L:98:ARG:HH11	2.27	0.43
11:A:204:G:H2'	11:A:205:A:H8	1.84	0.43
11:A:251:G:H1'	11:A:266:G:N7	2.34	0.43
11:A:301:G:H2'	11:A:302:G:H8	1.84	0.43
11:A:343:U:H2'	11:A:345:C:C5	2.54	0.43
1:D:2:ARG:O	1:D:4:LEU:CD1	2.67	0.43
5:L:47:ALA:O	5:L:49:ARG:HG3	2.19	0.43
6:O:81:ILE:HG13	6:O:82:GLU:CD	2.39	0.43
10:T:2:ASN:ND2	10:T:7:LYS:HG2	2.32	0.43
11:A:212:G:N3	11:A:213:G:C8	2.87	0.43
11:A:473:U:N3	11:A:474:G:C8	2.87	0.43
11:A:517:G:O6	11:A:532:A:C8	2.71	0.43
11:A:782:A:H5'	11:A:783:C:OP2	2.18	0.43
11:A:786:G:C6	11:A:787:A:N1	2.87	0.43
11:A:860:A:H2'	11:A:861:G:O4'	2.19	0.43
5:L:5:GLN:NE2	11:A:881:G:N7	2.64	0.42
5:L:23:LEU:HD13	5:L:94:TYR:CE1	2.54	0.42
7:P:70:ARG:O	7:P:74:LEU:CG	2.61	0.42
11:A:182:A:O2'	11:A:183:C:H3'	2.19	0.42
11:A:771:G:C6	11:A:809:G:C6	3.07	0.42
11:A:825:A:H2'	11:A:826:C:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:902:G:C4	11:A:903:G:C8	3.06	0.42
1:D:14:GLU:HG3	1:D:18:LEU:HD11	2.01	0.42
1:D:17:ASP:OD1	1:D:18:LEU:N	2.52	0.42
11:A:255:G:H2'	11:A:256:U:C6	2.54	0.42
11:A:284:C:H2'	11:A:285:C:H6	1.84	0.42
11:A:411:A:N1	11:A:430:A:C5	2.86	0.42
11:A:1519:A:C8	11:A:1520:C:C5	3.06	0.42
5:L:110:LYS:HB2	11:A:538:G:H5"	2.00	0.42
11:A:201:G:H2'	11:A:202:G:O4'	2.18	0.42
11:A:253:A:H2'	11:A:254:G:C8	2.54	0.42
11:A:398:U:H2'	11:A:399:G:C8	2.54	0.42
11:A:459:A:H61	11:A:472:U:H3	1.65	0.42
11:A:833:G:C6	11:A:834:U:C4	3.07	0.42
11:A:894:G:C4	11:A:895:G:C8	3.07	0.42
11:A:1519:A:O2'	11:A:1520:C:H6	2.02	0.42
5:L:56:LEU:HD11	5:L:81:ILE:HD11	2.01	0.42
11:A:76:G:O6	11:A:93:U:C4	2.72	0.42
11:A:130:A:H1'	11:A:263:A:O2'	2.20	0.42
11:A:461:A:O2'	11:A:467:U:OP1	2.32	0.42
11:A:829:G:O6	11:A:857:C:N4	2.31	0.42
11:A:896:C:H2'	11:A:897:C:C6	2.54	0.42
1:D:139:ASN:N	1:D:181:PHE:O	2.42	0.42
10:T:14:GLU:HG3	12:T:103:HOH:O	2.19	0.42
11:A:89:U:H2'	11:A:90:C:H6	1.81	0.42
11:A:441:A:H61	11:A:493:A:H61	1.62	0.42
11:A:455:G:H8	12:A:1652:HOH:O	1.97	0.42
11:A:560:A:H4'	11:A:561:U:H5"	2.01	0.42
11:A:688:G:C2	11:A:689:C:C5	3.08	0.42
1:D:53:GLN:O	1:D:56:GLU:HG3	2.20	0.42
4:K:13:LYS:NZ	4:K:35:ASP:OD2	2.38	0.42
6:O:14:PHE:CE2	6:O:84:LEU:HD13	2.54	0.42
8:Q:46:HIS:HB2	8:Q:70:LYS:HE3	2.02	0.42
11:A:28:A:H2'	11:A:29:U:O4'	2.20	0.42
11:A:155:A:N6	11:A:167:A:N6	2.68	0.42
11:A:680:C:H2'	11:A:681:A:C8	2.54	0.42
11:A:816:A:OP2	11:A:817:C:H2'	2.19	0.42
11:A:832:G:C2	11:A:833:G:C4	3.07	0.42
1:D:195:ASN:OD1	1:D:197:HIS:CE1	2.72	0.42
3:H:91:LEU:HD23	3:H:91:LEU:HA	1.89	0.42
7:P:6:LEU:HD22	7:P:17:TYR:HB3	2.01	0.42
8:Q:8:GLN:HE21	8:Q:78:VAL:HG21	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:T:55:PRO:HG3	11:A:193:C:H4'	2.01	0.42
11:A:202:G:H21	11:A:465:A:N6	2.18	0.42
11:A:205:A:C5	11:A:206:C:C5	3.08	0.42
11:A:264:C:H2'	11:A:265:G:O4'	2.20	0.42
11:A:398:U:H2'	11:A:399:G:H8	1.84	0.42
11:A:688:G:N2	11:A:700:G:H1'	2.34	0.42
1:D:33:ILE:CG2	1:D:34:GLU:N	2.69	0.42
1:D:160:LEU:HD12	1:D:160:LEU:O	2.20	0.42
11:A:160:A:H8	11:A:160:A:OP1	2.02	0.42
11:A:197:A:N1	11:A:220:G:O2'	2.46	0.42
11:A:459:A:H2'	11:A:460:A:C8	2.52	0.42
11:A:516:U:O4	11:A:532:A:C8	2.72	0.42
11:A:767:A:H2'	11:A:768:A:H8	1.85	0.42
11:A:1526:G:H2'	11:A:1527:U:H6	1.82	0.42
1:D:149:LYS:HG2	1:D:177:MET:HE3	2.02	0.42
6:O:32:THR:CG2	6:O:84:LEU:HD21	2.49	0.42
11:A:15:G:C4	11:A:16:A:C8	3.08	0.42
11:A:89:U:C2	11:A:90:C:C5	3.08	0.42
11:A:203:G:O2'	11:A:204:G:H8	2.02	0.42
11:A:409:U:H2'	11:A:410:G:C8	2.54	0.42
11:A:667:G:OP1	11:A:732:C:O2'	2.25	0.42
11:A:714:G:H2'	11:A:715:A:C8	2.54	0.42
11:A:810:C:H1'	11:A:899:C:H41	1.85	0.42
10:T:2:ASN:ND2	10:T:7:LYS:HE2	2.35	0.42
11:A:27:G:H2'	11:A:28:A:C8	2.53	0.42
11:A:88:U:O2'	11:A:89:U:H6	2.02	0.42
11:A:1507:A:O2'	11:A:1508:A:OP1	2.33	0.42
11:A:71:A:N1	11:A:99:C:O2'	2.49	0.41
11:A:749:A:H2'	11:A:750:C:O4'	2.19	0.41
11:A:779:C:OP2	11:A:780:A:N6	2.53	0.41
11:A:843:U:H2'	11:A:844:G:C4	2.55	0.41
2:F:37:HIS:CD2	2:F:38:ARG:HE	2.38	0.41
3:H:29:SER:HB3	11:A:589:U:H5"	2.02	0.41
5:L:33:CYS:N	5:L:54:VAL:HG23	2.32	0.41
8:Q:5:ARG:NH2	11:A:636:U:H5'	2.35	0.41
9:R:25:ILE:HG13	9:R:29:LYS:HE2	2.01	0.41
1:D:7:LYS:HB3	1:D:20:LEU:HD12	2.03	0.41
2:F:36:ILE:HD13	2:F:62:MET:HE2	2.00	0.41
2:F:57:ALA:HB3	2:F:59:TYR:CE1	2.55	0.41
6:O:22:GLY:O	11:A:751:U:H1'	2.21	0.41
6:O:75:ALA:HA	6:O:78:THR:HG22	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:335:C:O2'	11:A:336:A:P	2.78	0.41
11:A:712:A:C2	11:A:713:G:N2	2.89	0.41
2:F:49:TYR:OH	9:R:62:ARG:O	2.30	0.41
11:A:123:U:H2'	11:A:124:C:H6	1.85	0.41
11:A:155:A:C6	11:A:167:A:C6	3.09	0.41
11:A:517:G:C6	11:A:532:A:H8	2.38	0.41
11:A:573:A:O2'	11:A:574:A:H5'	2.20	0.41
11:A:669:G:N1	11:A:738:C:C4	2.88	0.41
11:A:832:G:C2	11:A:855:U:C2	3.09	0.41
3:H:102:VAL:HG13	3:H:125:ILE:HB	2.02	0.41
11:A:121:U:O2'	11:A:122:G:OP1	2.29	0.41
11:A:169:C:H2'	11:A:170:U:C6	2.55	0.41
11:A:263:A:H2'	11:A:264:C:C6	2.56	0.41
11:A:323:U:H2'	11:A:324:G:O4'	2.19	0.41
11:A:600:A:H2'	11:A:601:G:C8	2.55	0.41
11:A:785:G:C2	11:A:786:G:C5	3.08	0.41
11:A:1523:G:C4	11:A:1524:C:C5	3.08	0.41
2:F:75:GLU:HA	2:F:78:PHE:CD2	2.55	0.41
3:H:82:LEU:HD11	8:Q:33:TYR:O	2.19	0.41
11:A:13:U:C2	11:A:915:A:N7	2.89	0.41
11:A:683:G:H2'	11:A:684:U:C6	2.55	0.41
11:A:832:G:H2'	11:A:833:G:H8	1.84	0.41
11:A:1507:A:O2'	11:A:1508:A:P	2.79	0.41
1:D:118:SER:HB2	12:A:1727:HOH:O	2.19	0.41
5:L:97:VAL:HG12	5:L:100:ALA:CB	2.48	0.41
11:A:22:G:H2'	11:A:23:C:H6	1.86	0.41
11:A:96:U:H2'	11:A:97:G:H8	1.86	0.41
11:A:444:G:C6	11:A:490:C:N3	2.86	0.41
11:A:466:A:O5'	11:A:467:U:H5	2.02	0.41
11:A:771:G:C6	11:A:772:U:C4	3.08	0.41
11:A:838:G:C6	11:A:849:G:C5	3.09	0.41
1:D:103:ARG:C	1:D:105:GLY:H	2.24	0.41
2:F:26:THR:HG22	2:F:62:MET:HE1	2.03	0.41
2:F:68:GLN:HG2	11:A:739:C:P	2.61	0.41
5:L:98:ARG:NH2	5:L:106:VAL:HG12	2.33	0.41
11:A:390:U:H2'	11:A:391:G:C8	2.56	0.41
11:A:487:A:H2'	11:A:488:C:O4'	2.20	0.41
11:A:661:G:H2'	11:A:662:U:C6	2.56	0.41
11:A:665:A:H1'	11:A:733:G:O4'	2.21	0.41
11:A:707:U:H2'	11:A:708:C:C6	2.56	0.41
11:A:722:G:H3'	11:A:722:G:N3	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:780:A:H2	11:A:803:G:O6	2.03	0.41
11:A:806:C:H2'	11:A:807:A:H8	1.86	0.41
1:D:13:ARG:HD3	11:A:543:U:OP1	2.21	0.41
3:H:34:ALA:HB1	3:H:109:VAL:HB	2.02	0.41
3:H:115:ALA:HB1	3:H:120:LEU:O	2.21	0.41
4:K:79:LYS:O	4:K:104:PHE:HA	2.21	0.41
9:R:50:TYR:HA	9:R:53:GLN:OE1	2.21	0.41
10:T:60:GLN:OE1	10:T:60:GLN:HA	2.20	0.41
11:A:62:U:OP1	11:A:385:C:O2'	2.30	0.41
11:A:426:U:H2'	11:A:427:U:C6	2.56	0.41
11:A:573:A:N3	11:A:883:C:O2'	2.52	0.41
11:A:846:G:H3'	11:A:847:G:H8	1.85	0.41
3:H:80:PRO:O	11:A:878:A:H5"	2.21	0.41
11:A:75:G:C6	11:A:76:G:C5	3.08	0.41
11:A:334:C:C2'	11:A:335:C:H5'	2.51	0.41
1:D:4:LEU:CD2	11:A:406:G:H5'	2.50	0.40
1:D:120:LYS:HG3	11:A:439:U:H5'	2.02	0.40
4:K:41:LEU:HB3	4:K:76:TYR:CD2	2.56	0.40
5:L:55:ARG:HG2	5:L:55:ARG:NH1	2.36	0.40
5:L:71:HIS:HD2	5:L:72:ASN:N	2.18	0.40
11:A:295:C:H2'	11:A:296:U:O4'	2.21	0.40
11:A:399:G:H2'	11:A:400:C:C6	2.56	0.40
11:A:473:U:H2'	11:A:474:G:H5'	2.03	0.40
1:D:17:ASP:CG	1:D:27:ILE:HD11	2.41	0.40
3:H:4:ASP:OD1	3:H:80:PRO:HD3	2.21	0.40
5:L:107:LYS:HD3	5:L:107:LYS:N	2.35	0.40
6:O:4:THR:HG23	11:A:659:U:H5"	2.03	0.40
7:P:14:ARG:CB	7:P:42:ILE:HD11	2.51	0.40
11:A:79:G:C6	11:A:80:A:C6	3.09	0.40
11:A:180:U:C2'	11:A:181:A:H5'	2.50	0.40
11:A:679:C:H2'	11:A:680:C:C6	2.56	0.40
11:A:685:G:N1	11:A:704:A:OP2	2.45	0.40
1:D:8:LEU:HD23	1:D:31:CYS:HB2	2.02	0.40
1:D:10:LEU:CG	1:D:62:ARG:HD2	2.51	0.40
4:K:40:ALA:O	11:A:684:U:O2'	2.23	0.40
4:K:49:SER:HB2	4:K:68:ARG:NH1	2.36	0.40
8:Q:57:VAL:HG12	8:Q:78:VAL:CG2	2.52	0.40
9:R:51:GLN:HE22	9:R:54:LEU:HD23	1.85	0.40
11:A:76:G:N2	11:A:93:U:O2	2.41	0.40
11:A:204:G:C6	11:A:205:A:C5	3.10	0.40
11:A:211:G:N1	11:A:212:G:C4	2.89	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:A:640:A:O2'	11:A:641:U:H5'	2.22	0.40
11:A:673:A:H2'	11:A:674:G:H8	1.82	0.40
11:A:782:A:OP1	11:A:1522:U:H1'	2.21	0.40
1:D:169:TRP:CD2	1:D:185:PRO:HB3	2.56	0.40
3:H:2:MET:HE1	11:A:756:C:C1'	2.51	0.40
5:L:8:ARG:HH22	11:A:881:G:P	2.45	0.40
6:O:28:VAL:HG21	6:O:66:LEU:HD21	2.03	0.40
11:A:70:U:H5"	12:A:1698:HOH:O	2.21	0.40
11:A:83:C:H4'	11:A:84:U:C5	2.56	0.40
11:A:279:A:H5"	11:A:281:G:O4'	2.21	0.40
11:A:558:G:OP2	11:A:559:A:O2'	2.18	0.40
11:A:615:G:N2	12:A:1643:HOH:O	2.49	0.40
11:A:697:U:O3'	11:A:785:G:O2'	2.36	0.40
11:A:706:A:C6	11:A:707:U:C4	3.09	0.40
11:A:903:G:C4	11:A:904:U:C5	3.10	0.40
1:D:120:LYS:HE3	1:D:130:ASN:ND2	2.36	0.40
2:F:3:HIS:CD2	2:F:65:GLU:HG2	2.57	0.40
6:O:68:TYR:OH	11:A:752:G:H5"	2.22	0.40
9:R:24:ASP:O	9:R:28:LEU:HG	2.21	0.40
11:A:17:U:O2'	11:A:18:C:OP1	2.36	0.40
11:A:80:A:H2'	11:A:81:A:O4'	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	203/205 (99%)	177 (87%)	26 (13%)	0	100	100
2	F	98/135 (73%)	92 (94%)	6 (6%)	0	100	100
3	H	127/129 (98%)	117 (92%)	10 (8%)	0	100	100
4	K	93/128 (73%)	83 (89%)	10 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	L	121/123 (98%)	102 (84%)	19 (16%)	0	100	100
6	O	86/89 (97%)	82 (95%)	4 (5%)	0	100	100
7	P	80/82 (98%)	70 (88%)	10 (12%)	0	100	100
8	Q	78/83 (94%)	68 (87%)	10 (13%)	0	100	100
9	R	48/74 (65%)	41 (85%)	7 (15%)	0	100	100
10	T	83/86 (96%)	81 (98%)	2 (2%)	0	100	100
All	All	1017/1134 (90%)	913 (90%)	104 (10%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	172/172 (100%)	169 (98%)	3 (2%)	60	76
2	F	87/116 (75%)	86 (99%)	1 (1%)	73	84
3	H	104/104 (100%)	102 (98%)	2 (2%)	57	73
4	K	69/98 (70%)	68 (99%)	1 (1%)	67	79
5	L	103/103 (100%)	102 (99%)	1 (1%)	76	85
6	O	76/77 (99%)	76 (100%)	0	100	100
7	P	65/65 (100%)	65 (100%)	0	100	100
8	Q	74/77 (96%)	74 (100%)	0	100	100
9	R	43/64 (67%)	43 (100%)	0	100	100
10	T	65/65 (100%)	65 (100%)	0	100	100
All	All	858/941 (91%)	850 (99%)	8 (1%)	79	87

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	8	LEU

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Mol	Chain	Res	Type
1	D	44	LYS
1	D	150	LYS
2	F	35	LYS
3	H	88	LYS
3	H	113	ARG
4	K	55	ARG
5	L	95	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	99	ASN
1	D	197	HIS
2	F	63	ASN
4	K	100	ASN
5	L	71	HIS
6	O	41	HIS
6	O	45	HIS
8	Q	8	GLN
10	T	69	ASN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	A	960/1542 (62%)	259 (26%)	24 (2%)

All (259) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
11	A	9	G
11	A	14	U
11	A	18	C
11	A	20	U
11	A	25	C
11	A	32	A
11	A	33	A
11	A	35	G
11	A	39	G
11	A	44	A
11	A	47	C

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Mol	Chain	Res	Type
11	A	48	C
11	A	49	U
11	A	50	A
11	A	51	A
11	A	54	C
11	A	64	G
11	A	65	A
11	A	66	A
11	A	70	U
11	A	71	A
11	A	72	A
11	A	76	G
11	A	77	A
11	A	79	G
11	A	80	A
11	A	84	U
11	A	85	U
11	A	86	G
11	A	87	C
11	A	89	U
11	A	90	C
11	A	91	U
11	A	93	U
11	A	94	G
11	A	95	C
11	A	98	A
11	A	100	G
11	A	109	A
11	A	110	C
11	A	115	G
11	A	116	A
11	A	121	U
11	A	122	G
11	A	129	A
11	A	130	A
11	A	131	A
11	A	133	U
11	A	134	G
11	A	144	G
11	A	149	A
11	A	151	A
11	A	158	G

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Mol	Chain	Res	Type
11	A	159	G
11	A	164	G
11	A	173	U
11	A	177	G
11	A	181	A
11	A	182	A
11	A	183	C
11	A	184	G
11	A	195	A
11	A	196	A
11	A	197	A
11	A	205	A
11	A	209	U
11	A	211	G
11	A	222	C
11	A	225	C
11	A	239	U
11	A	240	G
11	A	243	A
11	A	244	U
11	A	245	U
11	A	247	G
11	A	251	G
11	A	258	G
11	A	266	G
11	A	267	C
11	A	279	A
11	A	280	C
11	A	289	G
11	A	296	U
11	A	298	A
11	A	301	G
11	A	305	G
11	A	306	A
11	A	321	A
11	A	323	U
11	A	328	C
11	A	329	A
11	A	332	G
11	A	335	C
11	A	336	A
11	A	338	A

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Mol	Chain	Res	Type
11	A	345	C
11	A	346	G
11	A	352	C
11	A	353	A
11	A	354	G
11	A	363	A
11	A	364	A
11	A	367	U
11	A	369	G
11	A	372	C
11	A	378	G
11	A	384	G
11	A	397	A
11	A	398	U
11	A	406	G
11	A	410	G
11	A	411	A
11	A	412	A
11	A	413	G
11	A	414	A
11	A	415	A
11	A	421	U
11	A	422	C
11	A	423	G
11	A	424	G
11	A	429	U
11	A	430	A
11	A	435	A
11	A	438	U
11	A	439	U
11	A	446	G
11	A	450	G
11	A	451	A
11	A	453	G
11	A	457	G
11	A	458	U
11	A	459	A
11	A	461	A
11	A	462	G
11	A	463	U
11	A	464	U
11	A	465	A

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Mol	Chain	Res	Type
11	A	466	A
11	A	467	U
11	A	468	A
11	A	473	U
11	A	475	C
11	A	482	A
11	A	484	G
11	A	486	U
11	A	488	C
11	A	492	C
11	A	493	A
11	A	495	A
11	A	508	U
11	A	509	A
11	A	511	C
11	A	517	G
11	A	518	C
11	A	521	G
11	A	522	C
11	A	527	G
11	A	532	A
11	A	533	A
11	A	536	C
11	A	537	G
11	A	547	A
11	A	560	A
11	A	564	C
11	A	572	A
11	A	573	A
11	A	576	C
11	A	577	G
11	A	588	G
11	A	596	A
11	A	607	A
11	A	615	G
11	A	618	C
11	A	619	U
11	A	620	C
11	A	642	A
11	A	650	G
11	A	653	U
11	A	656	G

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Mol	Chain	Res	Type
11	A	660	C
11	A	662	U
11	A	665	A
11	A	671	G
11	A	673	A
11	A	682	G
11	A	685	G
11	A	687	A
11	A	689	C
11	A	695	A
11	A	698	G
11	A	701	U
11	A	702	A
11	A	703	G
11	A	710	G
11	A	713	G
11	A	714	G
11	A	719	C
11	A	721	G
11	A	723	U
11	A	724	G
11	A	729	A
11	A	731	G
11	A	734	G
11	A	747	A
11	A	748	G
11	A	755	G
11	A	759	A
11	A	770	C
11	A	771	G
11	A	776	G
11	A	777	A
11	A	782	A
11	A	785	G
11	A	790	A
11	A	791	G
11	A	793	U
11	A	794	A
11	A	811	C
11	A	812	G
11	A	813	U
11	A	814	A

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Mol	Chain	Res	Type
11	A	815	A
11	A	816	A
11	A	817	C
11	A	818	G
11	A	820	U
11	A	821	G
11	A	828	U
11	A	829	G
11	A	835	U
11	A	836	G
11	A	841	C
11	A	842	U
11	A	843	U
11	A	844	G
11	A	846	G
11	A	847	G
11	A	871	U
11	A	874	G
11	A	876	C
11	A	900	A
11	A	902	G
11	A	904	U
11	A	914	A
11	A	923	A
11	A	928	G
11	A	1390	U
11	A	1502	A
11	A	1503	A
11	A	1504	G
11	A	1505	G
11	A	1507	A
11	A	1508	A
11	A	1509	C
11	A	1519	A
11	A	1520	C
11	A	1523	G
11	A	1529	G
11	A	1530	G

All (24) RNA pucker outliers are listed below:

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Mol	Chain	Res	Type
11	A	17	U
11	A	71	A
11	A	86	G
11	A	183	C
11	A	243	A
11	A	244	U
11	A	266	G
11	A	328	C
11	A	410	G
11	A	411	A
11	A	412	A
11	A	413	G
11	A	414	A
11	A	428	G
11	A	429	U
11	A	465	A
11	A	532	A
11	A	776	G
11	A	812	G
11	A	842	U
11	A	843	U
11	A	1507	A
11	A	1518	A
11	A	1528	U

5.4 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

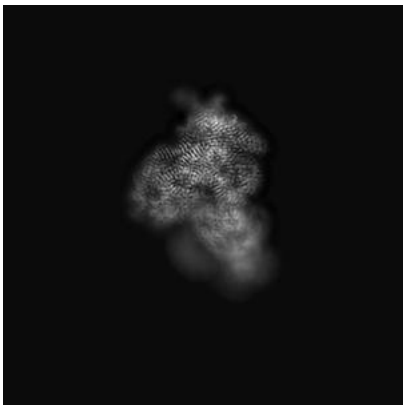
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-12916. These allow visual inspection of the internal detail of the map and identification of artifacts.

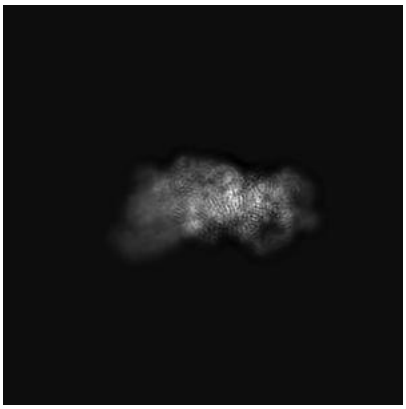
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

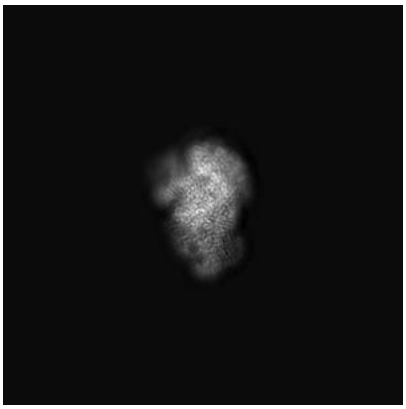
6.1.1 Primary map



X

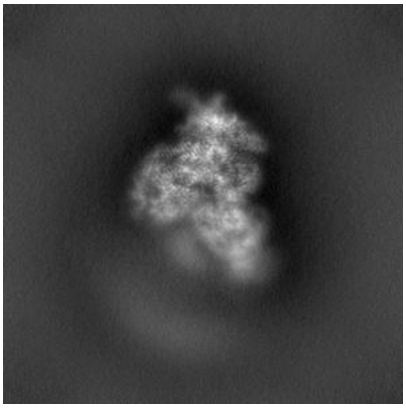


Y

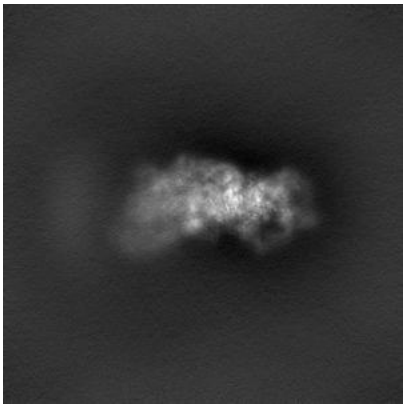


Z

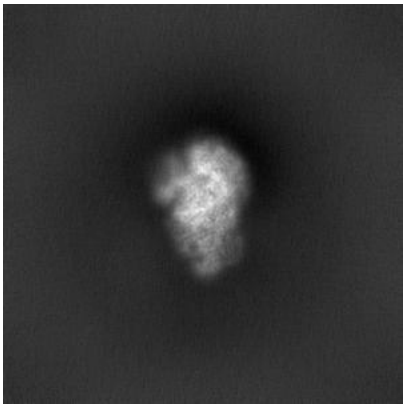
6.1.2 Raw map



X



Y

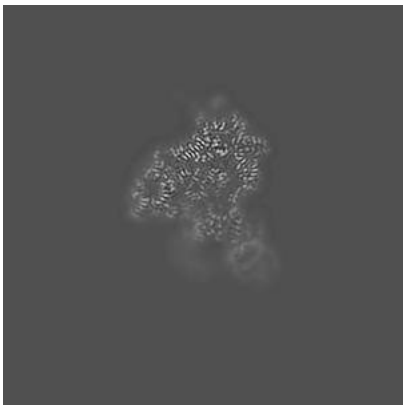


Z

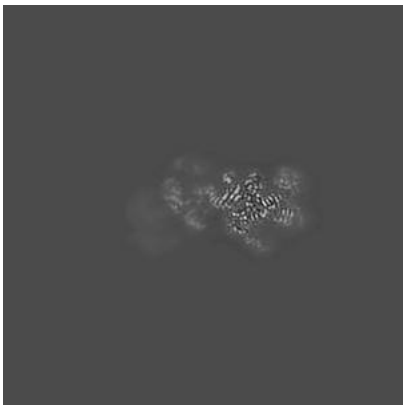
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

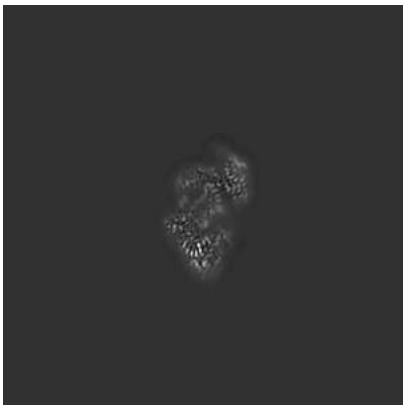
6.2.1 Primary map



X Index: 220

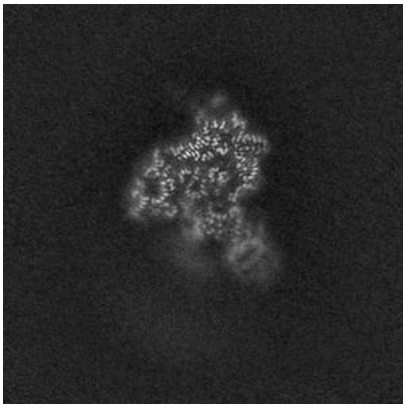


Y Index: 220

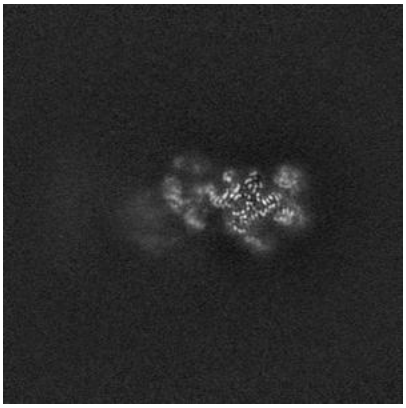


Z Index: 220

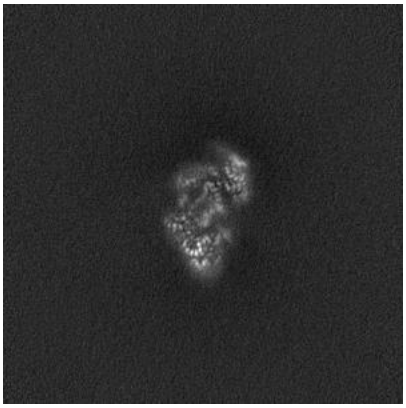
6.2.2 Raw map



X Index: 220



Y Index: 220

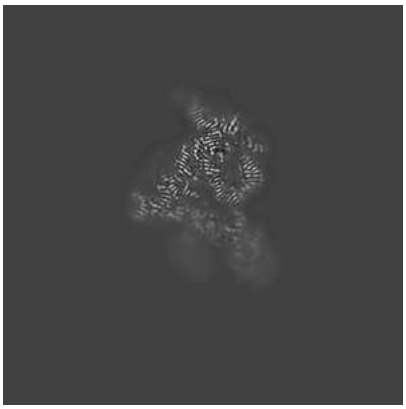


Z Index: 220

The images above show central slices of the map in three orthogonal directions.

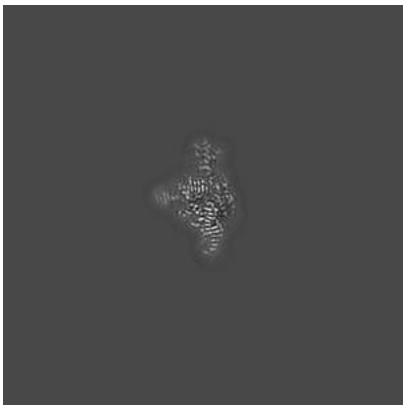
6.3 Largest variance slices (i)

6.3.1 Primary map



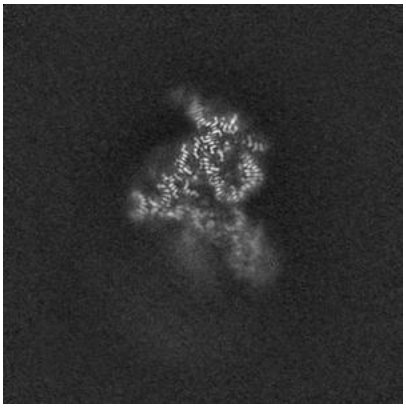
X Index: 213

Y Index: 238

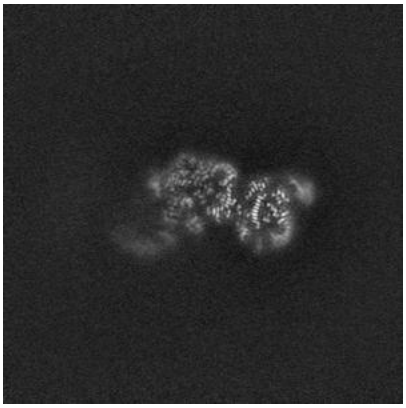


Z Index: 279

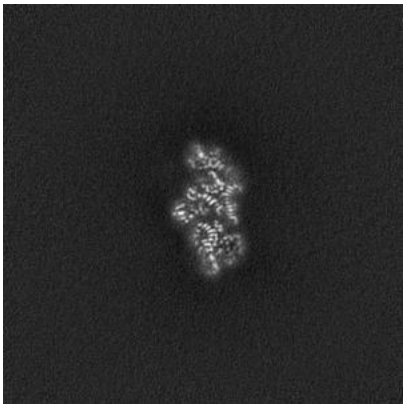
6.3.2 Raw map



X Index: 213



Y Index: 238

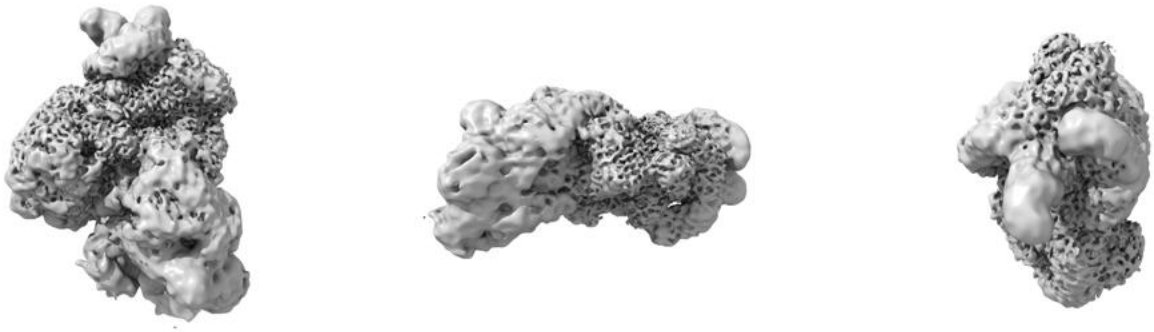


Z Index: 250

The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views (i)

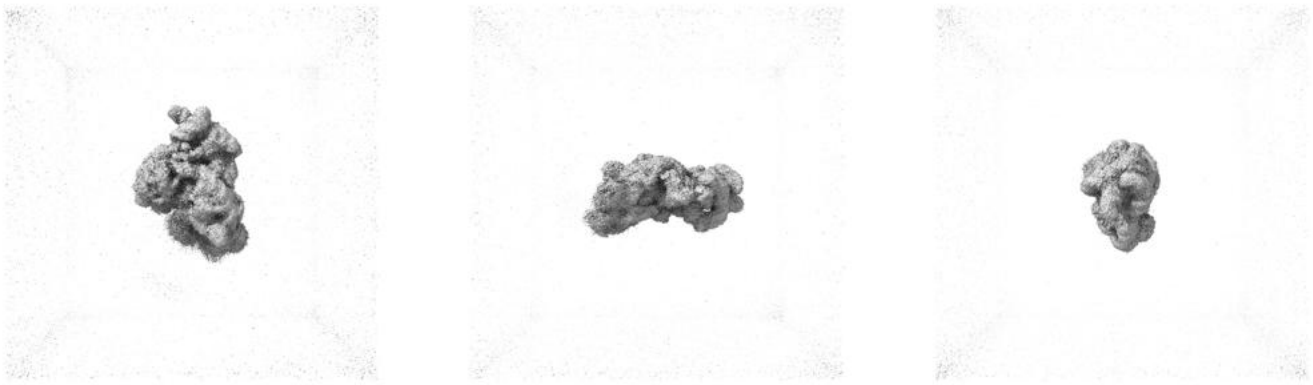
6.4.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.218. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 Raw map



X Y Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

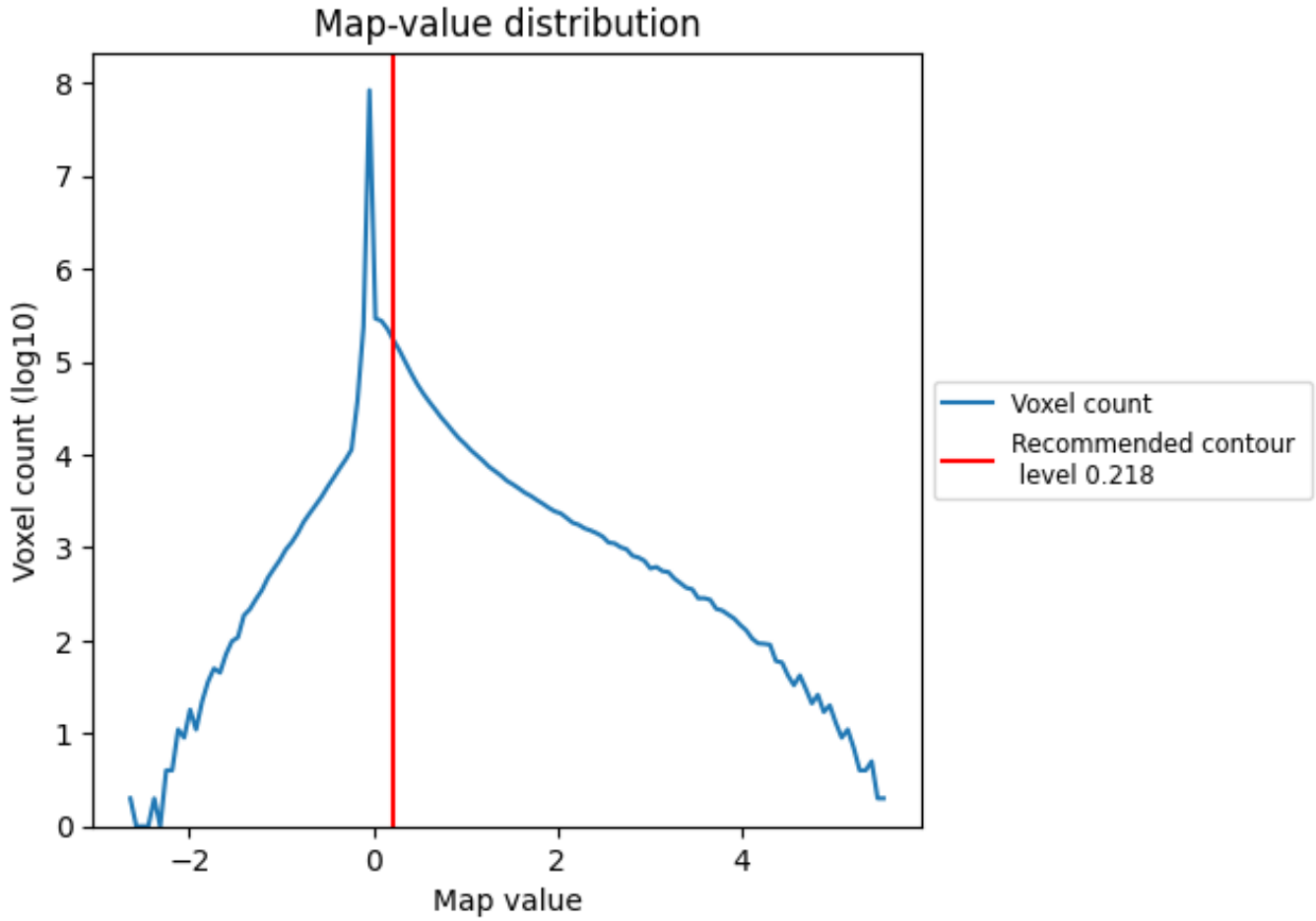
6.5 Mask visualisation (i)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis

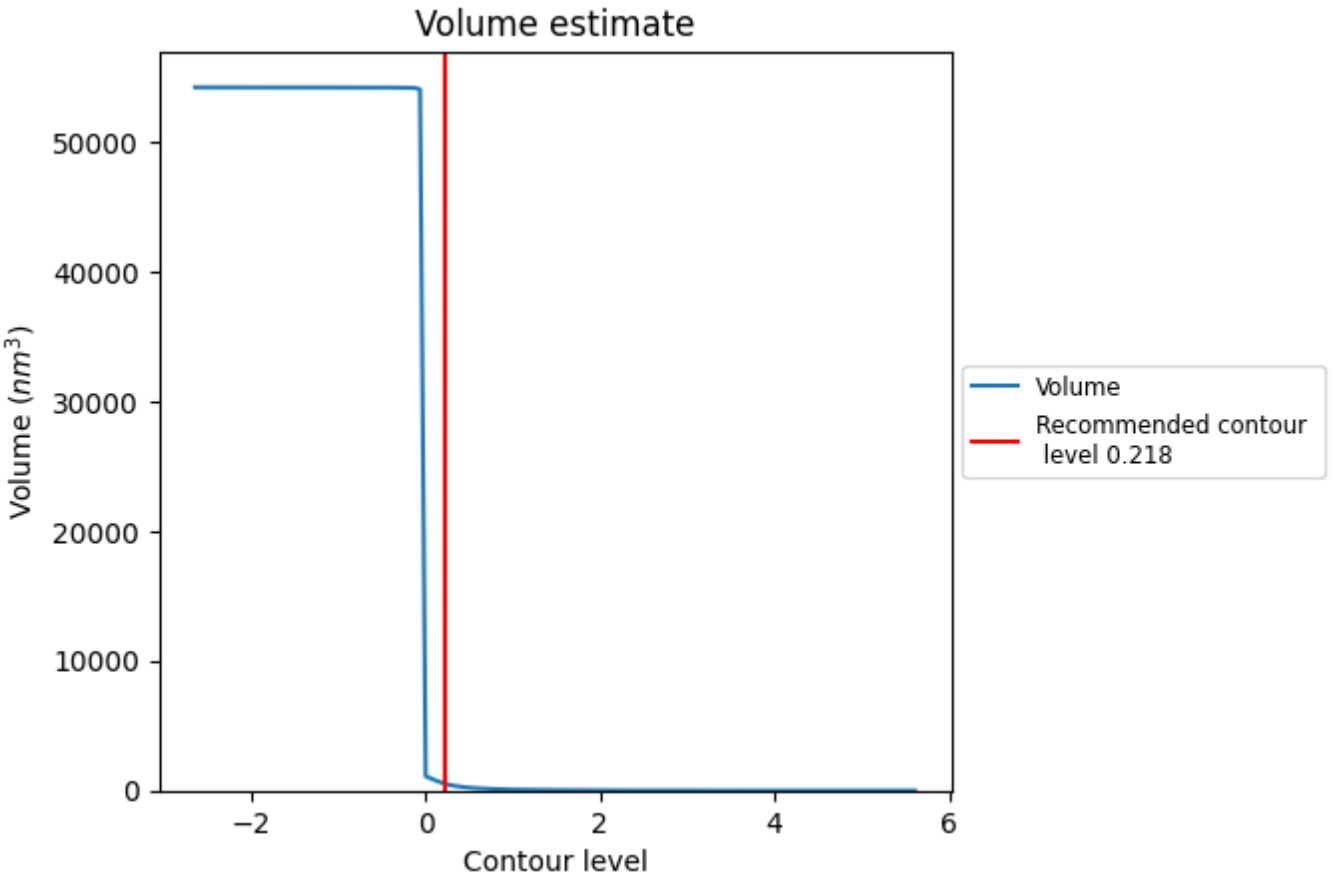
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

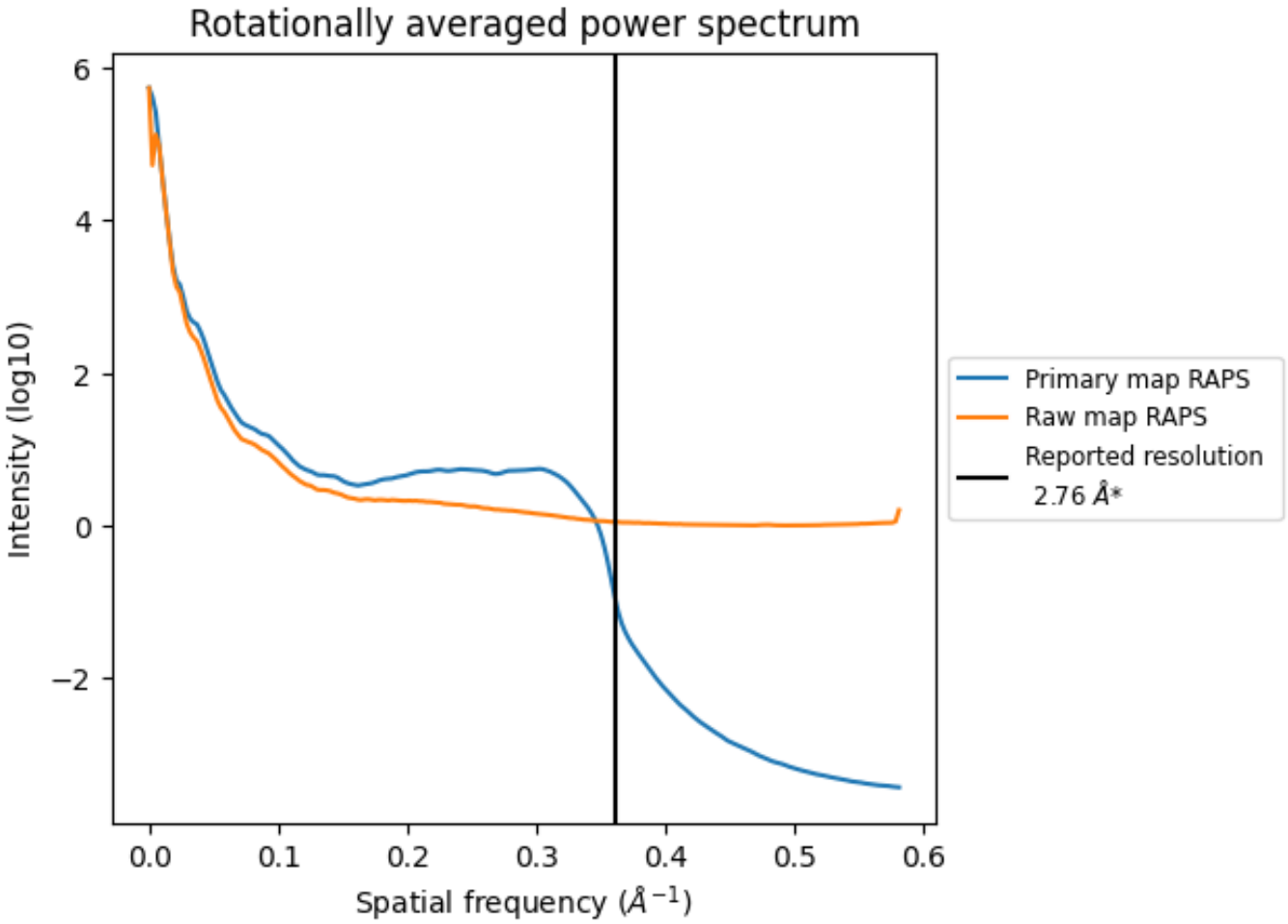
7.2 Volume estimate



The volume at the recommended contour level is 544 nm^3; this corresponds to an approximate mass of 491 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)

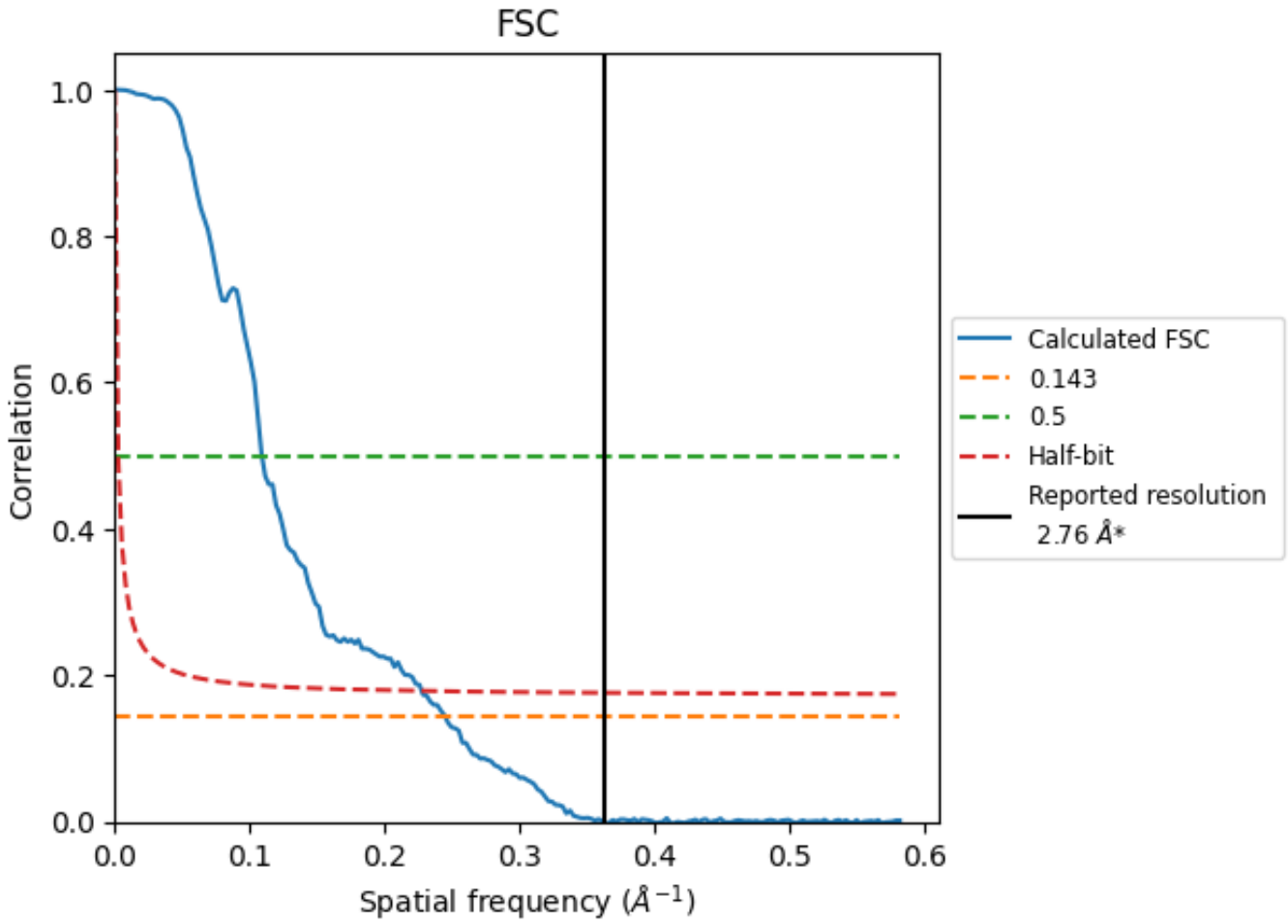


*Reported resolution corresponds to spatial frequency of 0.362 $Å^{-1}$

8 Fourier-Shell correlation

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC



*Reported resolution corresponds to spatial frequency of 0.362 Å^{-1}

8.2 Resolution estimates (i)

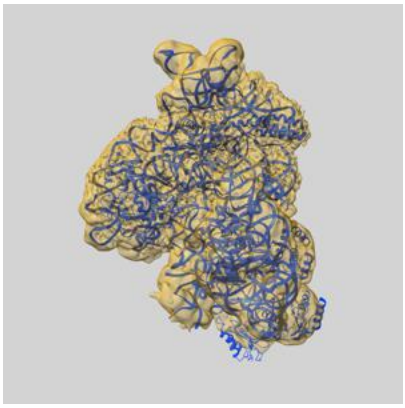
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.76	-	-
Author-provided FSC curve	-	-	-
Calculated*	4.08	9.17	4.40

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.08 differs from the reported value 2.76 by more than 10 %

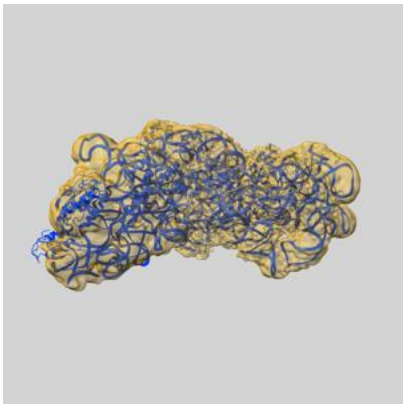
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-12916 and PDB model 7OI0. Per-residue inclusion information can be found in section 3 on page 7.

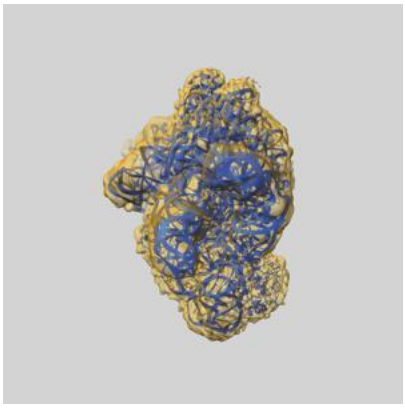
9.1 Map-model overlay



X



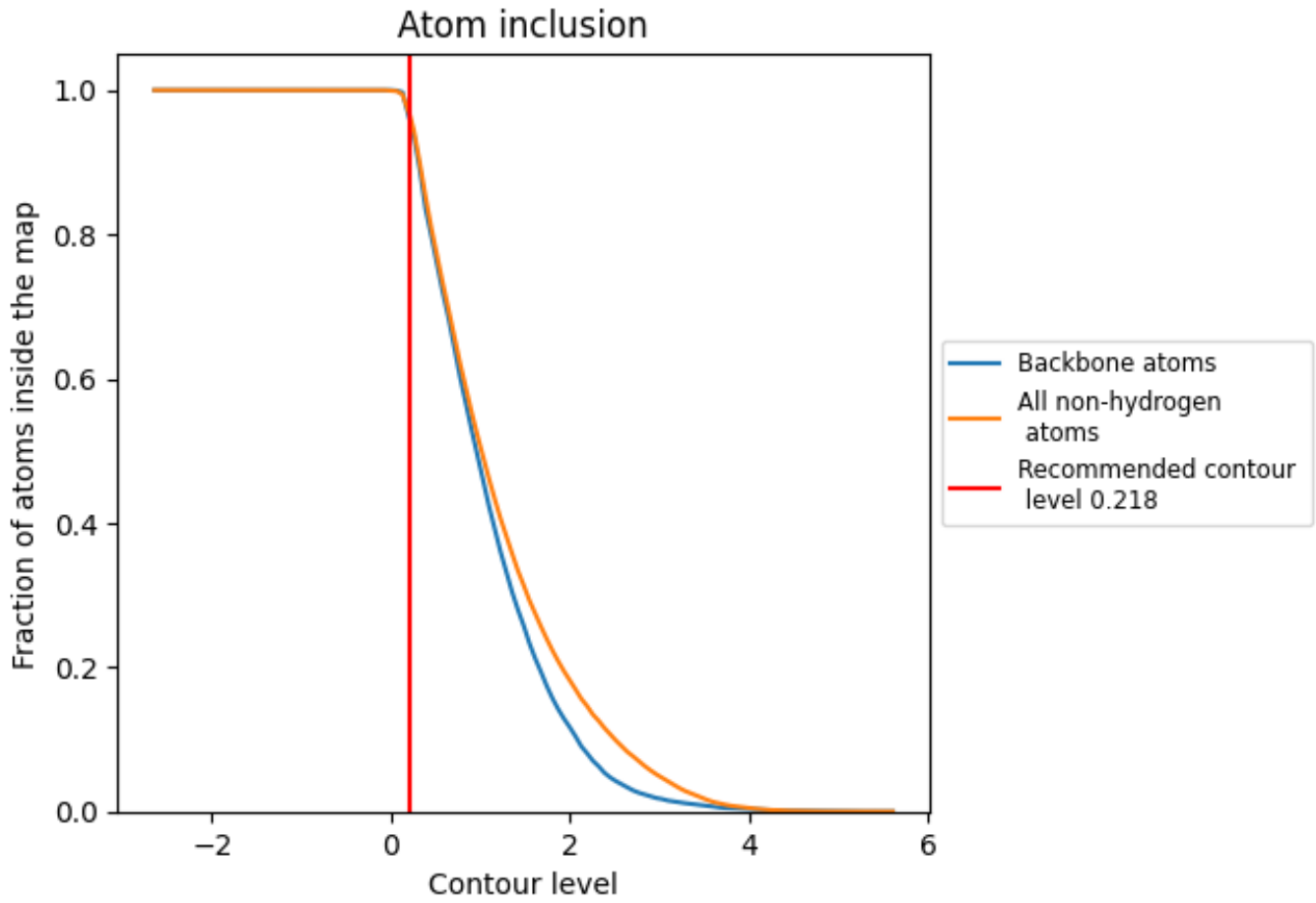
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.218 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Atom inclusion (i)



At the recommended contour level, 96% of all backbone atoms, 96% of all non-hydrogen atoms, are inside the map.